



Full wwPDB EM Validation Report ⓘ

Mar 22, 2025 – 06:59 am GMT

PDB ID : 9F5X
EMDB ID : EMD-50202
Title : Structure of the Chlamydomonas reinhardtii respiratory supercomplex I1 III2 IV2
Authors : Waltz, F.; Righetto, R.; Kotecha, A.; Engel, B.D.
Deposited on : 2024-04-30
Resolution : 2.82 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev117
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.5

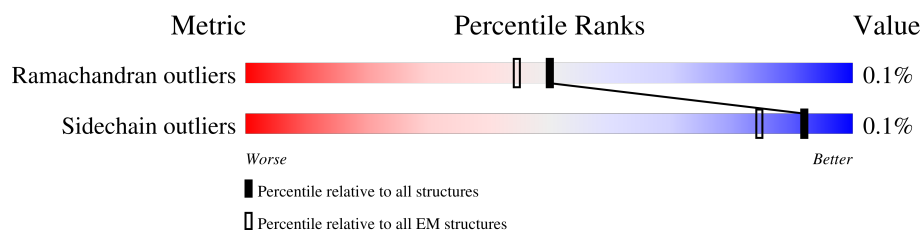
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.82 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



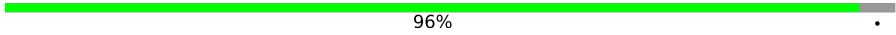
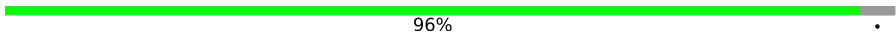
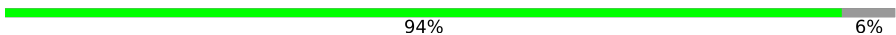








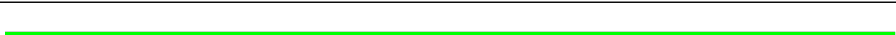

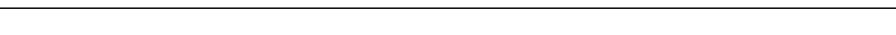
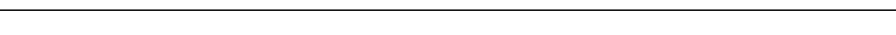
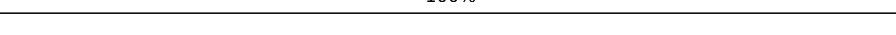
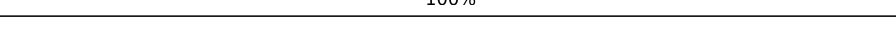
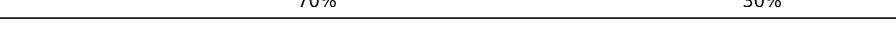

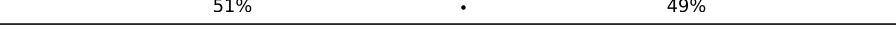
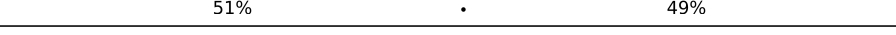




Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1A	381	98% ..
1	1B	381	98% ..
2	1C	262	79% 21%
2	1D	262	79% 21%
3	1E	314	77% 23%
3	1F	314	77% 23%
4	1G	60	98% .
4	1H	60	98% .
5	1I	69	99% .
5	1J	69	99% .




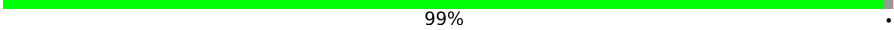
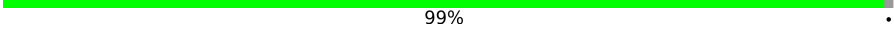






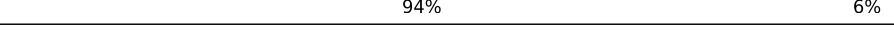


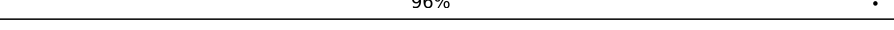




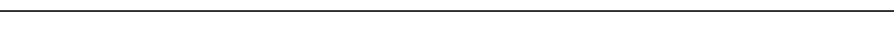

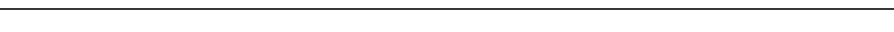
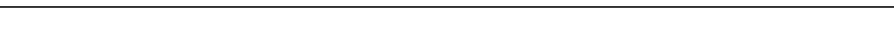


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Mol	Chain	Length	Quality of chain
6	1K	73	
6	1L	73	
7	1M	495	
7	1N	495	
8	1O	59	
8	1P	59	
9	1Q	485	
9	1S	485	
10	1R	123	
10	1T	123	
11	2A	504	
11	3A	504	
12	2B	284	
12	3B	284	
13	2C	153	
13	3C	153	
14	2D	382	
14	3D	382	
15	2E	175	
15	3E	175	
16	2F	96	
16	3F	96	
17	2G	125	
17	3G	125	
18	2H	148	


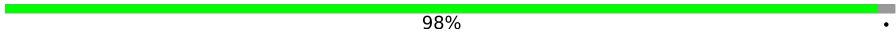
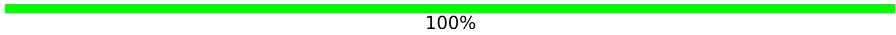

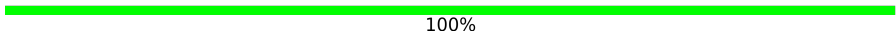

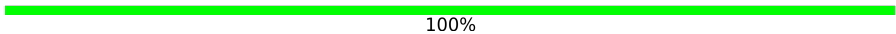
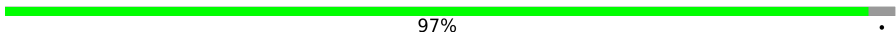







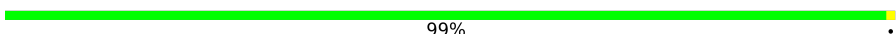
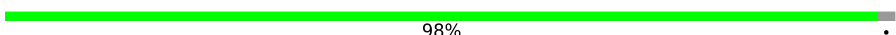


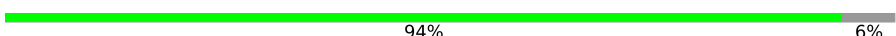
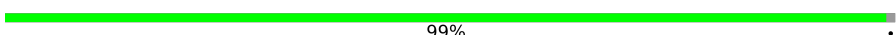
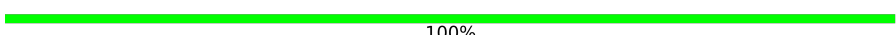
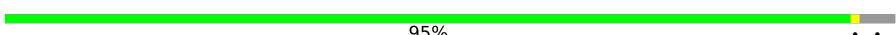
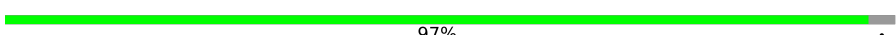
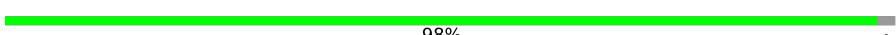
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Mol	Chain	Length	Quality of chain
18	3H	148	
19	2I	101	
19	3I	101	
20	2J	105	
20	3J	105	
21	2K	58	
21	3K	58	
22	2L	87	
22	3L	87	
23	A	282	
24	B	484	
25	C	733	
26	D	282	
27	E	467	
28	F	164	
29	G	231	
30	H	118	
31	I	165	
32	J	128	
32	r	128	
33	K	138	
34	L	187	
35	M	154	
36	N	156	
37	O	101	

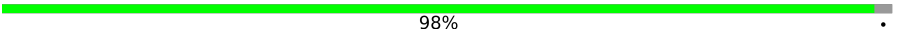


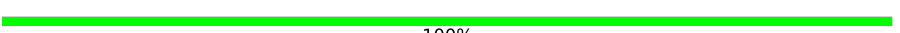


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Mol	Chain	Length	Quality of chain
38	P	397	
39	Q	292	
40	R	387	
41	S	279	
42	T	443	
43	U	227	
44	V	546	
45	W	162	
46	X	149	
47	Y	64	
48	Z	124	
49	a	129	
50	b	172	
51	c	67	
52	d	86	
53	e	219	
54	f	65	
55	g	55	
56	h	142	
57	i	81	
58	j	86	
59	k	117	
60	l	121	
61	m	142	
62	n	106	

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Mol	Chain	Length	Quality of chain
63	o	155	 98% .
64	p	130	 99% .
65	q	197	 80% 20%
66	s	312	 100%
67	t	279	 90% 9%
68	u	229	 100%
69	v	45	 100%
70	w	109	 59% 41%
71	x	157	 53% 47%
72	y	118	 97% .

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 137999 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Cytochrome b.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	376	Total	C	N	O	S	0	0
			2958	1984	466	491	17		
1	1B	376	Total	C	N	O	S	0	0
			2958	1984	466	491	17		

- Molecule 2 is a protein called Cytochrome b-c1 complex subunit Rieske, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1C	207	Total	C	N	O	S	0	0
			1602	1017	279	299	7		
2	1D	207	Total	C	N	O	S	0	0
			1602	1017	279	299	7		

- Molecule 3 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1E	243	Total	C	N	O	S	0	0
			1898	1204	326	356	12		
3	1F	243	Total	C	N	O	S	0	0
			1898	1204	326	356	12		

- Molecule 4 is a protein called Complex III subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	1G	59	Total	C	N	O	S	0	0
			486	316	79	88	3		
4	1H	59	Total	C	N	O	S	0	0
			486	316	79	88	3		

- Molecule 5 is a protein called Cytochrome b-c1 complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	1I	68	Total	C	N	O	S	0	0
			550	347	92	105	6		
5	1J	68	Total	C	N	O	S	0	0
			550	347	92	105	6		

- Molecule 6 is a protein called Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	1K	70	Total	C	N	O	S	0	0
			594	386	104	103	1		
6	1L	70	Total	C	N	O	S	0	0
			594	386	104	103	1		

- Molecule 7 is a protein called MPP-Beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	1M	464	Total	C	N	O	S	0	0
			3646	2290	641	696	19		
7	1N	464	Total	C	N	O	S	0	0
			3646	2290	641	696	19		

- Molecule 8 is a protein called Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	1O	48	Total	C	N	O	S	0	0
			371	249	61	60	1		
8	1P	48	Total	C	N	O	S	0	0
			371	249	61	60	1		

- Molecule 9 is a protein called Alpha-MPP.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	1Q	441	Total	C	N	O	S	0	0
			3204	2018	562	619	5		
9	1S	441	Total	C	N	O	S	0	0
			3204	2018	562	619	5		

- Molecule 10 is a protein called Cytochrome b-c1 complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	1R	122	Total	C	N	O	S	0	0
			980	617	178	183	2		
10	1T	122	Total	C	N	O	S	0	0
			980	617	178	183	2		

- Molecule 11 is a protein called Cytochrome c oxidase subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2A	504	Total	C	N	O	S	0	0
			3888	2600	618	643	27		
11	3A	504	Total	C	N	O	S	0	0
			3888	2600	618	643	27		

- Molecule 12 is a protein called Cytochrome c oxidase polypeptide II.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	2B	141	Total	C	N	O	S	0	0
			1169	774	188	201	6		
12	3B	141	Total	C	N	O	S	0	0
			1169	774	188	201	6		

- Molecule 13 is a protein called cytochrome-c oxidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	2C	153	Total	C	N	O	S	0	0
			1212	776	206	223	7		
13	3C	153	Total	C	N	O	S	0	0
			1212	776	206	223	7		

- Molecule 14 is a protein called Cytochrome c oxidase subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2D	266	Total	C	N	O	S	0	0
			2079	1373	334	351	21		
14	3D	266	Total	C	N	O	S	0	0
			2079	1373	334	351	21		

- Molecule 15 is a protein called Cox5b.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2E	90	Total	C	N	O	S	0	0
			737	478	114	144	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
15	3E	90	Total	C	N	O	S	0	0
			737	478	114	144	1		

- Molecule 16 is a protein called Cox5c.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	2F	86	Total	C	N	O	S	0	0
			706	456	122	126	2		
16	3F	86	Total	C	N	O	S	0	0
			706	456	122	126	2		

- Molecule 17 is a protein called Cox6a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	2G	91	Total	C	N	O	S	0	0
			733	484	120	124	5		
17	3G	91	Total	C	N	O	S	0	0
			733	484	120	124	5		

- Molecule 18 is a protein called Cox6b.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	2H	114	Total	C	N	O	S	0	0
			954	606	159	185	4		
18	3H	114	Total	C	N	O	S	0	0
			954	606	159	185	4		

- Molecule 19 is a protein called Cox7c.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	2I	72	Total	C	N	O	0	0
			594	393	98	103		
19	3I	72	Total	C	N	O	0	0
			594	393	98	103		

- Molecule 20 is a protein called Cytochrome c oxidase subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2J	104	Total	C	N	O	S	0	0
			816	522	144	147	3		
20	3J	104	Total	C	N	O	S	0	0
			816	522	144	147	3		

- Molecule 21 is a protein called Cox7a.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	2K	47	Total	C	N	O	0	0
			382	249	63	70		
21	3K	47	Total	C	N	O	0	0
			382	249	63	70		

- Molecule 22 is a protein called CoxIn.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2L	76	Total	C	N	O	S	0	0
			605	390	100	111	4		
22	3L	78	Total	C	N	O	S	0	0
			627	405	104	114	4		

- Molecule 23 is a protein called NADH:ubiquinone oxidoreductase 24 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	239	Total	C	N	O	S	0	0
			1839	1165	311	352	11		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	435	Total	C	N	O	S	0	0
			3331	2099	592	614	26		

- Molecule 25 is a protein called NADH:ubiquinone oxidoreductase 78 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	688	Total	C	N	O	S	0	0
			5175	3235	936	972	32		

- Molecule 26 is a protein called NADH:ubiquinone oxidoreductase 30kDa subunit domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	216	Total	C	N	O	S	0	0
			1790	1156	301	325	8		

- Molecule 27 is a protein called NADH:ubiquinone oxidoreductase 49 kD subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	383	Total	C	N	O	S	0	0
			3085	1971	537	554	23		

- Molecule 28 is a protein called NADH:ubiquinone oxidoreductase subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	157	Total	C	N	O	S	0	0
			1225	787	211	215	12		

- Molecule 29 is a protein called NADH:ubiquinone oxidoreductase subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	199	Total	C	N	O	S	0	0
			1615	1007	281	315	12		

- Molecule 30 is a protein called B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	90	Total	C	N	O	S	0	0
			750	486	129	132	3		

- Molecule 31 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	135	Total	C	N	O	S	0	0
			1044	661	173	208	2		

- Molecule 32 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	84	Total	C	N	O	S	0	0
			640	404	100	133	3		
32	r	88	Total	C	N	O	S	0	0
			663	419	104	137	3		

- Molecule 33 is a protein called NADH:ubiquinone oxidoreductase B14 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	119	Total	C	N	O	S	0	0
			986	640	173	168	5		

- Molecule 34 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	164	Total	C	N	O	S	0	0
			1275	803	221	245	6		

- Molecule 35 is a protein called NADH:ubiquinone oxidoreductase 13 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	121	Total	C	N	O	S	0	0
			913	582	150	178	3		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	150	Total	C	N	O	S	0	0
			1235	791	214	227	3		

- Molecule 37 is a protein called NADH:ubiquinone oxidoreductase B8 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	100	Total	C	N	O	S	0	0
			761	471	138	147	5		

- Molecule 38 is a protein called Putative NADH:ubiquinone oxidoreductase 39 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	363	Total	C	N	O	S	0	0
			2823	1793	489	527	14		

- Molecule 39 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	286	Total	C	N	O	S	0	0
			2179	1448	338	374	19		

- Molecule 40 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	387	Total	C	N	O	S	0	0
			3014	2026	467	496	25		

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	134	Total	C	N	O	S	0	0
			1071	715	159	192	5		

- Molecule 42 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	443	Total	C	N	O	S	0	0
			3434	2321	526	557	30		

- Molecule 43 is a protein called NADH dehydrogenase subunit 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	105	Total	C	N	O	S	0	0
			805	524	124	146	11		

- Molecule 44 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	546	Total	C	N	O	S	0	0
			4152	2731	668	716	37		

- Molecule 45 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	157	Total	C	N	O	S	0	0
			1210	820	180	201	9		

- Molecule 46 is a protein called ASH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	125	Total	C	N	O	S	0	0
			1037	685	168	178	6		

- Molecule 47 is a protein called P9.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	54	Total	C	N	O	S	0	0
			405	256	74	74	1		

- Molecule 48 is a protein called KFYI.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	107	Total	C	N	O	S	0	0
			861	555	149	152	5		

- Molecule 49 is a protein called AGGG.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	82	Total	C	N	O	S	0	0
			674	440	109	123	2		

- Molecule 50 is a protein called ESSS.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	b	144	Total	C	N	O	S	0	0
			1169	756	192	214	7		

- Molecule 51 is a protein called B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	c	59	Total	C	N	O	S	0	0
			453	298	71	79	5		

- Molecule 52 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	d	85	Total	C	N	O	S	0	0
			699	456	120	120	3		

- Molecule 53 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	e	218	Total	C	N	O	S	0	0
			1639	1055	279	297	8		

- Molecule 54 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	f	64	Total	C	N	O	S	0	0
			532	345	93	92	2		

- Molecule 55 is a protein called Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5

kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	g	50	Total	C	N	O	S	0	0
			416	277	73	65	1		

- Molecule 56 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	h	108	Total	C	N	O	S	0	0
			915	597	157	159	2		

- Molecule 57 is a protein called NADH:ubiquinone oxidoreductase 15 kDa subunit-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	i	76	Total	C	N	O	S	0	0
			633	387	122	116	8		

- Molecule 58 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	j	85	Total	C	N	O	S	0	0
			712	449	131	125	7		

- Molecule 59 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	k	117	Total	C	N	O	S	0	0
			984	631	176	173	4		

- Molecule 60 is a protein called NADH:ubiquinone oxidoreductase 20,9 kD-like subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	l	116	Total	C	N	O	S	0	0
			904	589	150	161	4		

- Molecule 61 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	m	138	Total	C	N	O	S	0	0
			1126	724	205	193	4		

- Molecule 62 is a protein called Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	n	104	Total	C	N	O	S	0	0
			864	547	152	159	6		

- Molecule 63 is a protein called Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	o	152	Total	C	N	O	S	0	0
			1240	771	238	228	3		

- Molecule 64 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	p	129	Total	C	N	O	S	0	0
			1069	670	192	204	3		

- Molecule 65 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 19 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	q	157	Total	C	N	O	S	0	0
			1268	818	217	229	4		

- Molecule 66 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	s	312	Total	C	N	O	S	0	0
			2302	1451	407	435	9		

- Molecule 67 is a protein called CAG2 - CA-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	t	253	Total	C	N	O	S	0	0
			1997	1268	357	367	5		

- Molecule 68 is a protein called CAG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	u	228	Total	C	N	O	S	0	0
			1698	1063	300	327	8		

- Molecule 69 is a protein called P10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	v	45	Total	C	N	O	S	0	0
			361	233	61	66	1		

- Molecule 70 is a protein called Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa sub-unit.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	w	64	Total	C	N	O	S	0	0
			508	334	78	91	5		

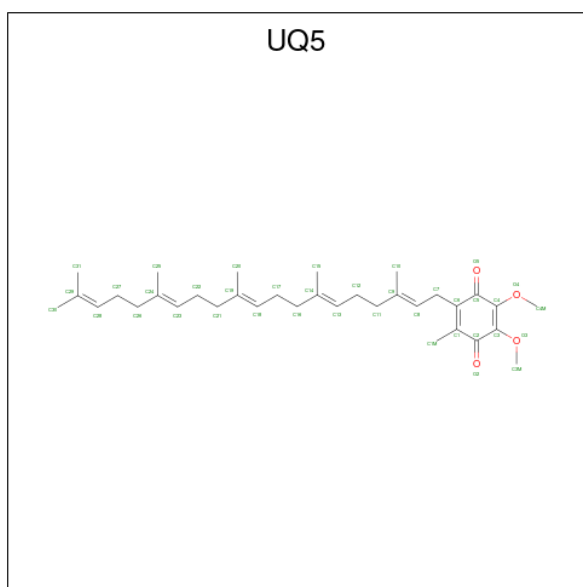
- Molecule 71 is a protein called NUOP8.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	x	83	Total	C	N	O	S	0	0
			699	467	110	121	1		

- Molecule 72 is a protein called NUOP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	y	114	Total	C	N	O	S	0	0
			932	615	154	161	2		

- Molecule 73 is 2,3-DIMETHOXY-5-METHYL-6-(3,11,15,19-TETRAMETHYL-EICOSA-2,6,10,14,18-PENTAENYL)-[1,4]BENZOQUINONE (three-letter code: UQ5) (formula: $C_{34}H_{50}O_4$).



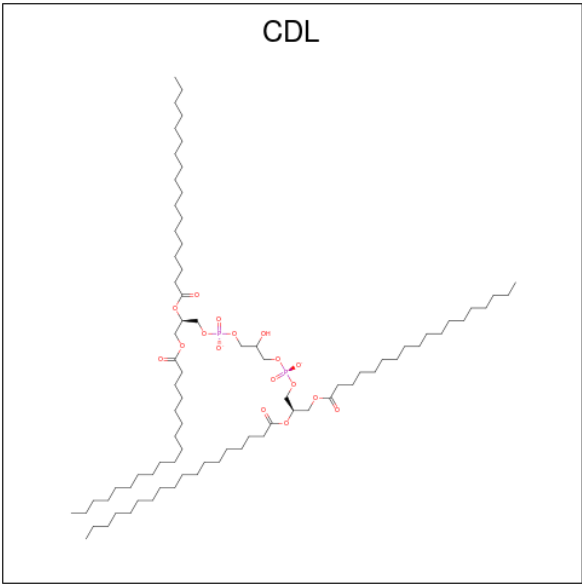
Mol	Chain	Residues	Atoms			AltConf
73	1A	1	Total	C	O	0
			38	34	4	
73	1A	1	Total	C	O	0
			38	34	4	
73	1B	1	Total	C	O	0
			38	34	4	
73	1B	1	Total	C	O	0
			38	34	4	
73	Q	1	Total	C	O	0
			38	34	4	

- Molecule 74 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



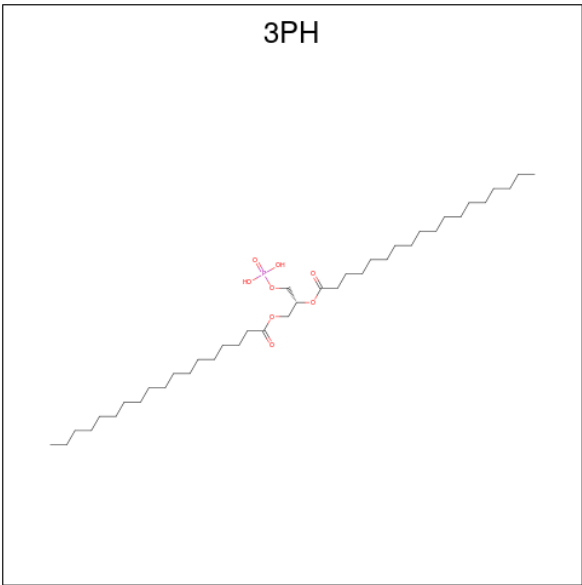
Mol	Chain	Residues	Atoms					AltConf
74	1A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
74	1B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 75 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms				AltConf
75	1A	1	Total	C	O	P	0
			59	40	17	2	
75	1B	1	Total	C	O	P	0
			64	45	17	2	
75	1B	1	Total	C	O	P	0
			71	52	17	2	
75	1E	1	Total	C	O	P	0
			53	34	17	2	
75	1F	1	Total	C	O	P	0
			56	37	17	2	
75	1K	1	Total	C	O	P	0
			79	60	17	2	
75	1L	1	Total	C	O	P	0
			59	40	17	2	
75	1M	1	Total	C	O	P	0
			54	35	17	2	
75	R	1	Total	C	O	P	0
			63	44	17	2	
75	V	1	Total	C	O	P	0
			64	45	17	2	
75	W	1	Total	C	O	P	0
			95	76	17	2	
75	h	1	Total	C	O	P	0
			77	58	17	2	
75	u	1	Total	C	O	P	0
			83	64	17	2	
75	u	1	Total	C	O	P	0
			71	52	17	2	
75	x	1	Total	C	O	P	0
			92	73	17	2	
75	y	1	Total	C	O	P	0
			55	36	17	2	

- Molecule 76 is 1,2-DIACYL-GLYCEROL-3-SN-PHOSPHATE (three-letter code: 3PH) (formula: C₃₉H₇₇O₈P).



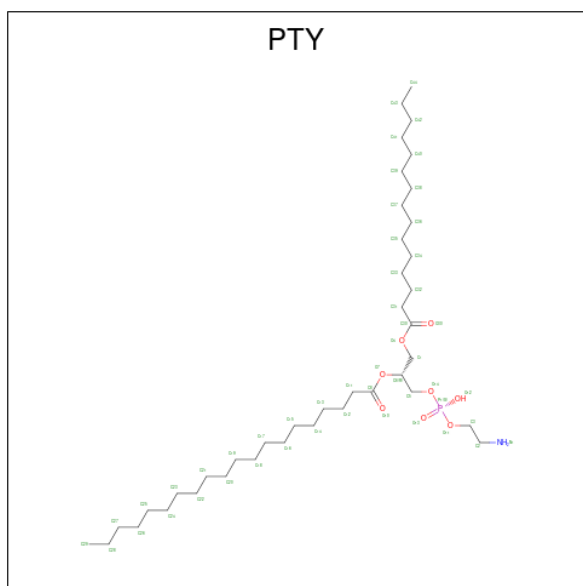
Mol	Chain	Residues	Atoms				AltConf
76	1A	1	Total	C	O	P	0
			31	22	8	1	
76	1B	1	Total	C	O	P	0
			48	39	8	1	
76	1B	1	Total	C	O	P	0
			48	39	8	1	
76	1E	1	Total	C	O	P	0
			40	31	8	1	
76	1K	1	Total	C	O	P	0
			48	39	8	1	
76	1R	1	Total	C	O	P	0
			37	28	8	1	
76	2D	1	Total	C	O	P	0
			32	23	8	1	
76	2I	1	Total	C	O	P	0
			42	33	8	1	
76	3D	1	Total	C	O	P	0
			32	23	8	1	
76	3I	1	Total	C	O	P	0
			42	33	8	1	
76	R	1	Total	C	O	P	0
			32	23	8	1	
76	S	1	Total	C	O	P	0
			37	28	8	1	
76	V	1	Total	C	O	P	0
			42	33	8	1	
76	V	1	Total	C	O	P	0
			41	32	8	1	

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Mol	Chain	Residues	Atoms				AltConf
76	c	1	Total	C	O	P	0
			48	39	8	1	
76	g	1	Total	C	O	P	0
			37	28	8	1	
76	h	1	Total	C	O	P	0
			45	36	8	1	
76	w	1	Total	C	O	P	0
			45	36	8	1	
76	y	1	Total	C	O	P	0
			32	23	8	1	

- Molecule 77 is PHOSPHATIDYLETHANOLAMINE (three-letter code: PTY) (formula: $C_{40}H_{80}NO_8P$).



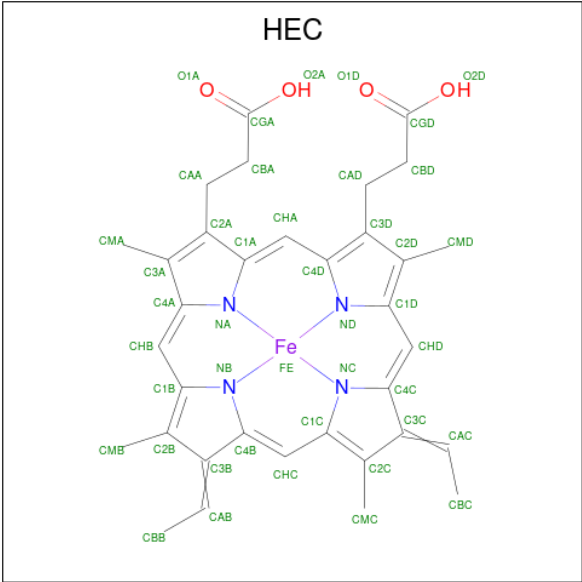
Mol	Chain	Residues	Atoms					AltConf
77	1E	1	Total 34	C 24	N 1	O 8	P 1	0
77	1F	1	Total 38	C 28	N 1	O 8	P 1	0
77	2D	1	Total 35	C 25	N 1	O 8	P 1	0
77	2F	1	Total 34	C 24	N 1	O 8	P 1	0
77	3D	1	Total 35	C 25	N 1	O 8	P 1	0
77	3F	1	Total 34	C 24	N 1	O 8	P 1	0

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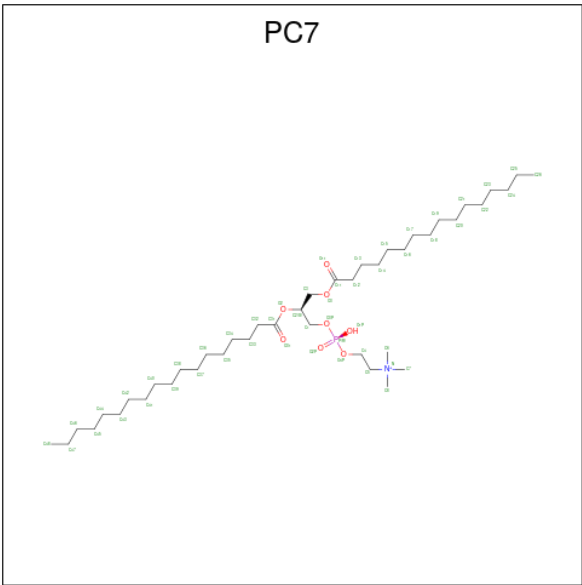
Mol	Chain	Residues	Atoms					AltConf
77	G	1	Total	C	N	O	P	0
			43	33	1	8	1	
77	R	1	Total	C	N	O	P	0
			34	24	1	8	1	
77	R	1	Total	C	N	O	P	0
			44	34	1	8	1	
77	R	1	Total	C	N	O	P	0
			40	30	1	8	1	
77	S	1	Total	C	N	O	P	0
			46	36	1	8	1	
77	T	1	Total	C	N	O	P	0
			50	40	1	8	1	
77	T	1	Total	C	N	O	P	0
			28	18	1	8	1	
77	T	1	Total	C	N	O	P	0
			26	16	1	8	1	
77	V	1	Total	C	N	O	P	0
			40	30	1	8	1	
77	V	1	Total	C	N	O	P	0
			50	40	1	8	1	
77	V	1	Total	C	N	O	P	0
			35	25	1	8	1	
77	e	1	Total	C	N	O	P	0
			25	15	1	8	1	
77	e	1	Total	C	N	O	P	0
			43	33	1	8	1	
77	h	1	Total	C	N	O	P	0
			46	36	1	8	1	
77	x	1	Total	C	N	O	P	0
			50	40	1	8	1	

- Molecule 78 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms					AltConf
78	1E	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
78	1F	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 79 is (7S)-4-HYDROXY-N,N,N-TRIMETHYL-9-OXO-7-[(PALMITOYLOXY)METHYL]-3,5,8-TRIOXA-4-PHOSPHAHEXACOSAN-1-AMINIUM 4-OXIDE (three-letter code: PC7) (formula: C₄₂H₈₅NO₈P).



Mol	Chain	Residues	Atoms					AltConf
79	1G	1	Total	C	N	O	P	0
			36	26	1	8	1	

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Mol	Chain	Residues	Atoms					AltConf
79	1H	1	Total	C	N	O	P	0
			39	29	1	8	1	
79	2A	1	Total	C	N	O	P	0
			27	17	1	8	1	
79	3A	1	Total	C	N	O	P	0
			27	17	1	8	1	
79	Q	1	Total	C	N	O	P	0
			33	23	1	8	1	
79	R	1	Total	C	N	O	P	0
			44	34	1	8	1	
79	T	1	Total	C	N	O	P	0
			52	42	1	8	1	
79	u	1	Total	C	N	O	P	0
			42	32	1	8	1	

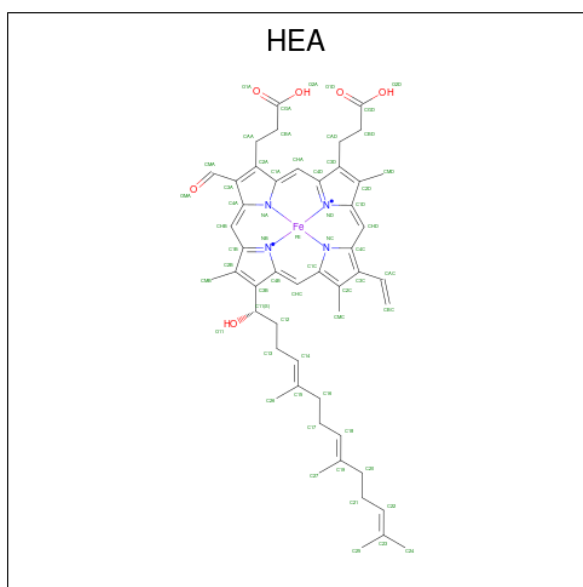
- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
80	1M	1	Total	Zn	0
			1	1	
80	1N	1	Total	Zn	0
			1	1	
80	s	1	Total	Zn	0
			1	1	

- Molecule 81 is (1S)-2-{{[(2R)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL STEARATE (three-letter code: PGT) (formula: C₄₀H₇₉O₁₀P).



- Molecule 82 is HEME-A (three-letter code: HEA) (formula: $\text{C}_{49}\text{H}_{56}\text{FeN}_4\text{O}_6$).



Mol	Chain	Residues	Atoms					AltConf
82	2A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	2A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0
82	3A	1	Total 60	C 49	Fe 1	N 4	O 6	0

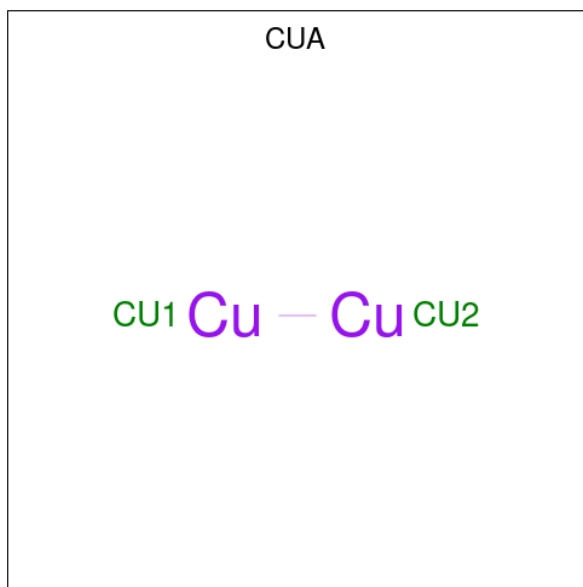
- Molecule 83 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		AltConf
83	2A	1	Total	Cu	0
			1	1	
83	3A	1	Total	Cu	0
			1	1	

- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

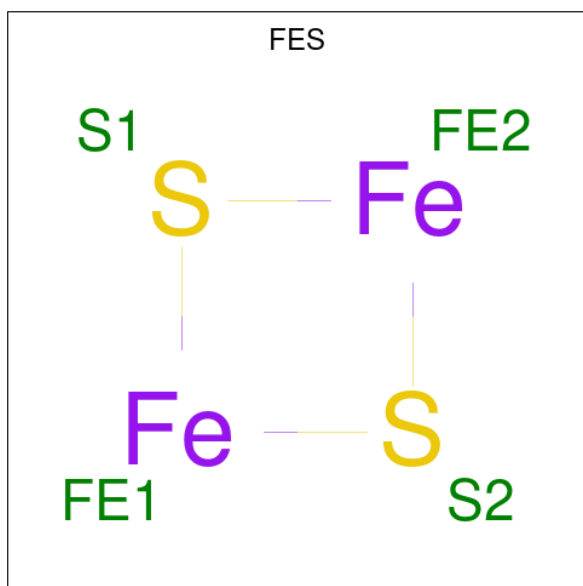
Mol	Chain	Residues	Atoms		AltConf
84	2A	1	Total	Mg	0
			1	1	
84	3A	1	Total	Mg	0
			1	1	

- Molecule 85 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



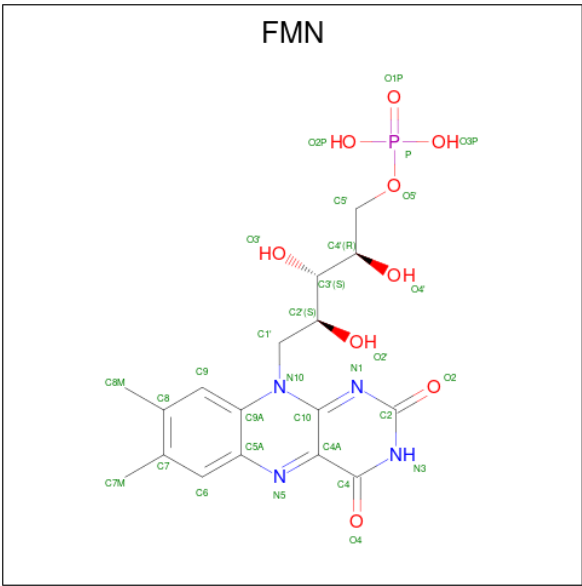
Mol	Chain	Residues	Atoms		AltConf
85	2C	1	Total	Cu	0
			2	2	
85	3C	1	Total	Cu	0
			2	2	

- Molecule 86 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



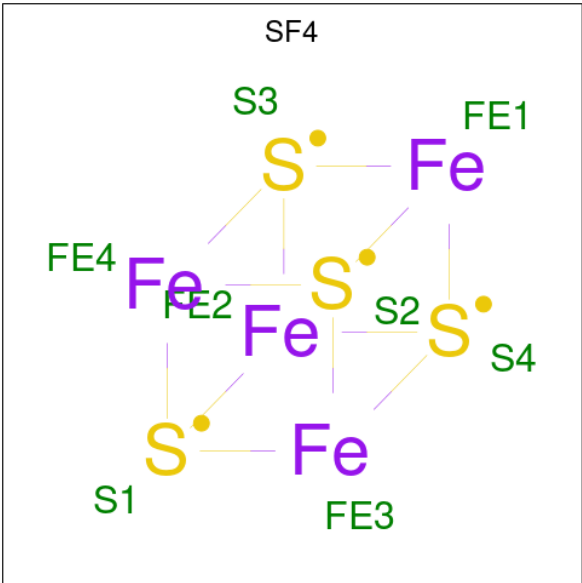
Mol	Chain	Residues	Atoms			AltConf
86	A	1	Total	Fe	S	0
			4	2	2	
86	C	1	Total	Fe	S	0
			4	2	2	

- Molecule 87 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					AltConf
87	B	1	Total	C	N	O	P	0
			31	17	4	9	1	

- Molecule 88 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



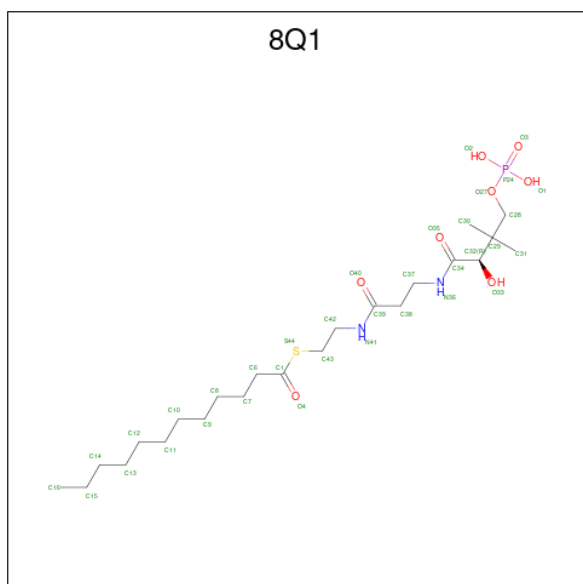
Mol	Chain	Residues	Atoms			AltConf
88	B	1	Total	Fe	S	0
			8	4	4	
88	C	1	Total	Fe	S	0
			8	4	4	

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Mol	Chain	Residues	Atoms			AltConf
88	C	1	Total	Fe	S	0
			8	4	4	
88	F	1	Total	Fe	S	0
			8	4	4	
88	G	1	Total	Fe	S	0
			8	4	4	
88	G	1	Total	Fe	S	0
			8	4	4	

- Molecule 89 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (three-letter code: 8Q1) (formula: C₂₃H₄₅N₂O₈PS).



Mol	Chain	Residues	Atoms						AltConf
89	J	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
89	r	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 90 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					AltConf
90	P	1	Total 48	C 21	N 7	O 17	P 3	0

- Molecule 91 is CROTONYL COENZYME A (three-letter code: COO) (formula: $\text{C}_{25}\text{H}_{40}\text{N}_7\text{O}_{17}\text{P}_3\text{S}$).



Mol	Chain	Residues	Atoms						AltConf
91	s	1	Total	C	N	O	P	S	0
			53	25	7	17	3	1	

- Molecule 92 is water.

Mol	Chain	Residues	Atoms		AltConf
92	1A	48	Total 48	O 48	0
92	1B	52	Total 52	O 52	0
92	1C	13	Total 13	O 13	0
92	1D	12	Total 12	O 12	0
92	1E	51	Total 51	O 51	0
92	1F	34	Total 34	O 34	0
92	1G	7	Total 7	O 7	0
92	1H	9	Total 9	O 9	0
92	1I	11	Total 11	O 11	0
92	1J	3	Total 3	O 3	0
92	1K	12	Total 12	O 12	0
92	1L	12	Total 12	O 12	0
92	1M	76	Total 76	O 76	0
92	1N	74	Total 74	O 74	0
92	1O	4	Total 4	O 4	0
92	1P	6	Total 6	O 6	0
92	1Q	27	Total 27	O 27	0
92	1R	32	Total 32	O 32	0
92	1S	29	Total 29	O 29	0
92	1T	28	Total 28	O 28	0
92	A	24	Total 24	O 24	0
92	B	66	Total 66	O 66	0

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Mol	Chain	Residues	Atoms		AltConf
92	C	168	Total 168	O 168	0
92	D	66	Total 66	O 66	0
92	E	87	Total 87	O 87	0
92	F	39	Total 39	O 39	0
92	G	62	Total 62	O 62	0
92	H	16	Total 16	O 16	0
92	I	19	Total 19	O 19	0
92	K	16	Total 16	O 16	0
92	L	68	Total 68	O 68	0
92	M	30	Total 30	O 30	0
92	N	53	Total 53	O 53	0
92	O	6	Total 6	O 6	0
92	P	69	Total 69	O 69	0
92	Q	24	Total 24	O 24	0
92	R	64	Total 64	O 64	0
92	S	22	Total 22	O 22	0
92	T	85	Total 85	O 85	0
92	U	14	Total 14	O 14	0
92	V	99	Total 99	O 99	0
92	W	25	Total 25	O 25	0
92	X	50	Total 50	O 50	0

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Mol	Chain	Residues	Atoms		AltConf
92	Y	4	Total 4	O 4	0
92	Z	20	Total 20	O 20	0
92	a	6	Total 6	O 6	0
92	b	24	Total 24	O 24	0
92	c	1	Total 1	O 1	0
92	d	12	Total 12	O 12	0
92	e	55	Total 55	O 55	0
92	f	10	Total 10	O 10	0
92	g	7	Total 7	O 7	0
92	h	38	Total 38	O 38	0
92	i	30	Total 30	O 30	0
92	j	29	Total 29	O 29	0
92	k	51	Total 51	O 51	0
92	l	17	Total 17	O 17	0
92	m	32	Total 32	O 32	0
92	n	7	Total 7	O 7	0
92	o	51	Total 51	O 51	0
92	p	21	Total 21	O 21	0
92	q	24	Total 24	O 24	0
92	r	12	Total 12	O 12	0
92	s	39	Total 39	O 39	0

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Mol	Chain	Residues	Atoms		AltConf
92	t	55	Total 55	O 55	0
92	u	41	Total 41	O 41	0
92	v	2	Total 2	O 2	0
92	w	16	Total 16	O 16	0
92	x	22	Total 22	O 22	0
92	y	29	Total 29	O 29	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Cytochrome b

Chain 1A:  98% ..




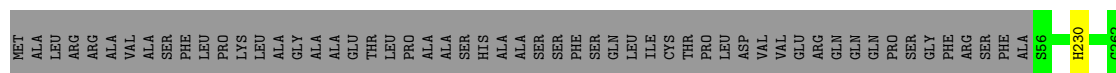
- Molecule 1: Cytochrome b

Chain 1B:  98% ..




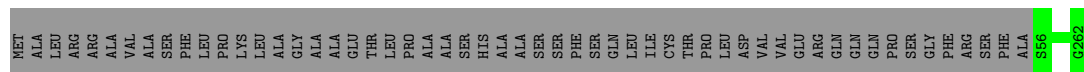
- Molecule 2: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain 1C:  79% 21%




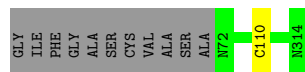
- Molecule 2: Cytochrome b-c1 complex subunit Rieske, mitochondrial

Chain 1D:  79% 21%




- Molecule 3: Cytochrome c1

Chain 1E:  77% 23%



- Molecule 3: Cytochrome c1

Chain 1F:  77% 23%

MET ARG THR LEU ARG SER LEU GLY LYS GLY LEU GLY CYS ALA GLU ALA THR SER SER ARG VAL ALA GLN THR MET PRO VAL ALA MET SER SER THR SER ALA ASP ALA GLU PRO THR SER LYS ALA ALA HIS THR ALA ALA LEU GLY VAL MET ALA

GLY ILE PHE GLY ALA SER CYS VAL ALA SER ALA N72 R314

- Molecule 4: Complex III subunit 9

Chain 1G:  98%

MET Y2 T60

- Molecule 4: Complex III subunit 9

Chain 1H:  98%

MET Y2 T60

- Molecule 5: Cytochrome b-c1 complex subunit 6

Chain 1I:  99%

MET Y2 K69

- Molecule 5: Cytochrome b-c1 complex subunit 6

Chain 1J:  99%

MET Y2 K69

- Molecule 6: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8

Chain 1K:  96%

MET ALA PRO R4 Y73

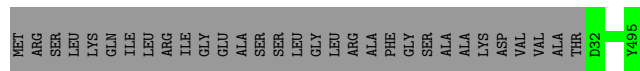
- Molecule 6: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 8

Chain 1L:  96%

MET ALA PRO R4 Y73

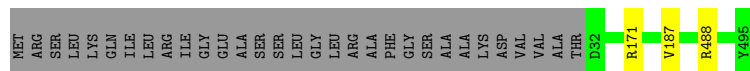
- Molecule 7: MPP-Beta

Chain 1M:  94% 6%




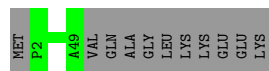
- Molecule 7: MPP-Beta

Chain 1N:  93% 6%




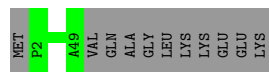
- Molecule 8: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10

Chain 1O:  81% 19%



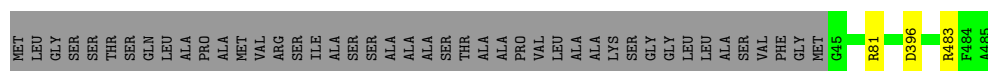
- Molecule 8: Mitochondrial ubiquinol-cytochrome c oxidoreductase subunit 10

Chain 1P:  81% 19%




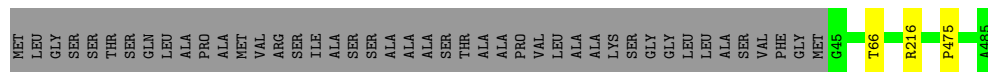
- Molecule 9: Alpha-MPP

Chain 1Q:  90% 9%

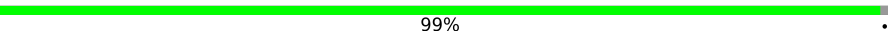


- Molecule 9: Alpha-MPP

Chain 1S:  90% 9%



- Molecule 10: Cytochrome b-c1 complex subunit 7

Chain 1R:  99%



- Molecule 10: Cytochrome b-c1 complex subunit 7

Chain 1T:  99%



- Molecule 11: Cytochrome c oxidase subunit 1

Chain 2A:  100%



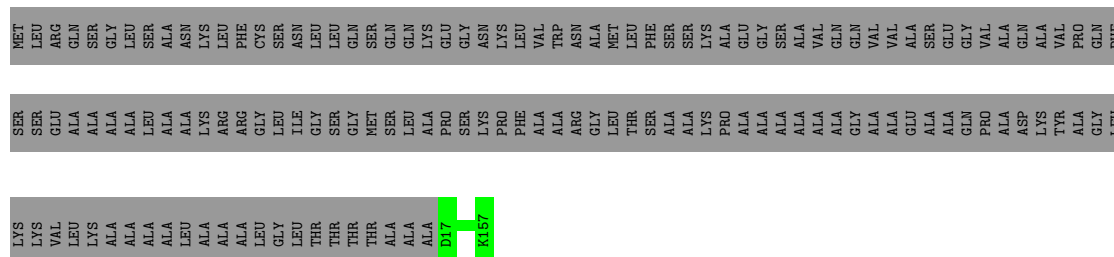
- Molecule 11: Cytochrome c oxidase subunit 1

Chain 3A:  100%



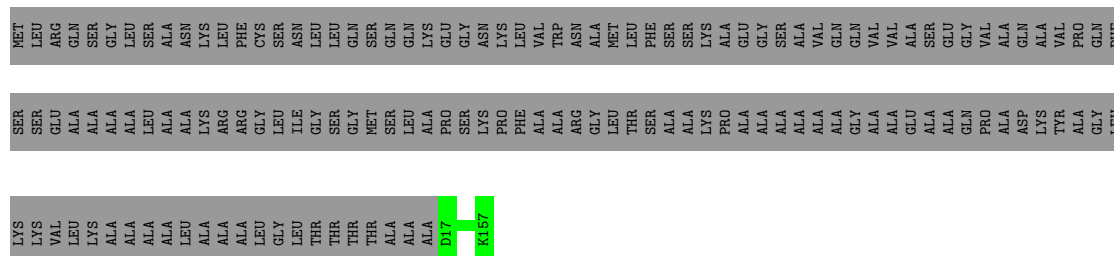
- Molecule 12: Cytochrome c oxidase polypeptide II

Chain 2B:  50%



- Molecule 12: Cytochrome c oxidase polypeptide II

Chain 3B:  50%



- Molecule 13: cytochrome-c oxidase

Chain 2C:  100%

There are no outlier residues recorded for this chain.

- Molecule 13: cytochrome-c oxidase

Chain 3C:  100%

There are no outlier residues recorded for this chain.

- Molecule 14: Cytochrome c oxidase subunit 3

Chain 2D:  70% 30%

MET ARG SER GLN LEU LEU ARG PHE LEU THR ARG ALA PRO GLY PHE SER ASN GLN GLU GLY LEU GLN ALA LEU LEU ARG ALA GLY THR SER GLY GLU ALA SER SER LEU GLN SER SER PHE GLY ARG GLN ASN GLY THR PRO ARG GLY HIS MET THR LEU ALA ALA SER GLY PHE SER ASN GLN GLU ASP ASP LYS LYS GLN ALA GLU ALA PRO THR THR GLY ALA LEU LEU ALA GLN GLU PRO GLN VAL GLY SER PRO ASN ALA LEU SER SER ALA ALA PHE GLY ARG GLN ARG GLN ASN THR MET GLY SER HIS GLY LEU ALA ALA GLY PHE GLY LYS MET ALA

LEU PRO LEU SER PHE GLN GLY HIS LEU LEU MET THR THR LEU ALA ALA SER GLY PHE SER ASN GLN GLU ASP ASP LYS LYS GLN ALA GLU ALA PRO THR THR GLY ALA LEU LEU ALA GLN GLU PRO GLN VAL GLY SER PRO ASN ALA LEU SER SER ALA ALA PHE GLY ARG GLN ARG GLN ASN THR MET GLY SER HIS GLY LEU ALA ALA GLY PHE GLY LYS MET ALA

- Molecule 14: Cytochrome c oxidase subunit 3

Chain 3D:  70% 30%

MET ARG SER GLN LEU LEU ARG PHE LEU THR ARG ALA PRO GLY PHE SER ASN GLN GLU GLY LEU GLN ALA LEU LEU ARG ALA GLY THR SER GLY GLU ALA SER SER LEU GLN SER SER PHE GLY ARG GLN ARG GLN ASN THR MET GLY SER HIS GLY LEU ALA ALA GLY PHE GLY LYS MET ALA

LEU PRO LEU SER PHE GLN GLY HIS LEU LEU MET THR THR LEU ALA ALA SER GLY PHE SER ASN GLN GLU ASP ASP LYS LYS GLN ALA GLU ALA PRO THR THR GLY ALA LEU LEU ALA GLN GLU PRO GLN VAL GLY SER PRO ASN ALA LEU SER SER ALA ALA PHE GLY ARG GLN ARG GLN ASN THR MET GLY SER HIS GLY LEU ALA ALA GLY PHE GLY LYS MET ALA

- Molecule 15: Cox5b

Chain 2E:  51% 49%

MET ASN ARG SER GLN LEU LEU GLY ALA LEU LEU SER GLY LEU LEU LEU ALA ARG ALA ALA ARG ALA THR THR CYS SER SER ARG ARG TRP THR THR ALA ALA VAL GLY VAL PRO PRO ALA GLU LEU SER SER ALA ALA VAL GLY ILE VAL GLY GLN GLU PHE PHE ALA ALA GLN THR THR ARG SER SER HIS THR THR CYS GLN GLY MET ALA

PRO ALA GLU ALA LYS PRO SER ALA LEU LEU ALA ALA PRO PRO ARG LYS Y15 Y28 G104 GLY ASP LYS ALA LYS LYS LYS

- Molecule 15: Cox5b

Chain 3E:  51% 49%

MET ASN ARG SER GLN LEU LEU GLY ALA LEU LEU SER GLY LEU LEU LEU ALA ARG ALA ALA ARG ALA THR THR CYS SER SER ARG ARG TRP THR THR ALA ALA VAL GLY VAL PRO PRO ALA GLU LEU SER SER ALA ALA VAL GLY ILE VAL GLY GLN GLU PHE PHE ALA ALA GLN THR THR ARG SER SER HIS THR THR CYS GLN GLY MET ALA

PRO ALA GLU ALA LYS PRO SER ALA LEU LEU ALA ALA PRO PRO ARG LYS Y15 Y28 G104 GLY ASP LYS ALA LYS LYS LYS

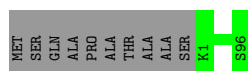
- Molecule 16: Cox5c

Chain 2F:  90% 10%

MET SER GLN ALA PRO THR ALA SER K1 S96

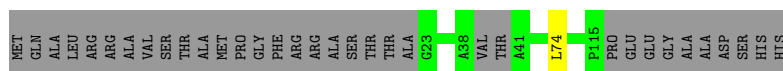
- Molecule 16: Cox5c

Chain 3F:  90% 10%



- Molecule 17: Cox6a

Chain 2G:  72% 27%




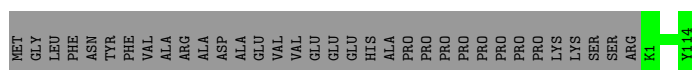
- Molecule 17: Cox6a

Chain 3G:  70% 27%




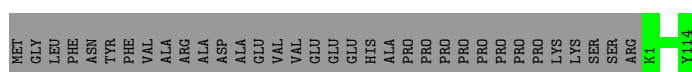
- Molecule 18: Cox6b

Chain 2H:  77% 23%



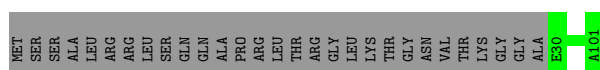
- Molecule 18: Cox6b

Chain 3H:  77% 23%



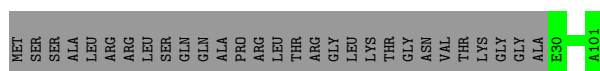
- Molecule 19: Cox7c

Chain 2I:  71% 29%



- Molecule 19: Cox7c

Chain 3I:  71% 29%



- Molecule 20: Cytochrome c oxidase subunit

Chain 2J:  99% .



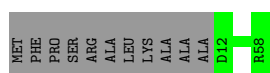
- Molecule 20: Cytochrome c oxidase subunit

Chain 3J: 99%



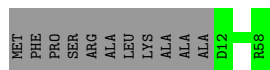
- Molecule 21: Cox7a

Chain 2K: 81% 19%



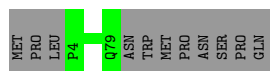
- Molecule 21: Cox7a

Chain 3K: 81% 19%



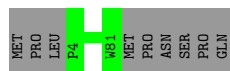
- Molecule 22: CoxIn

Chain 2L: 87% 13%



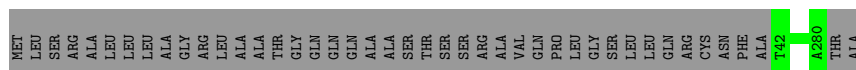
- Molecule 22: CoxIn

Chain 3L: 90% 10%



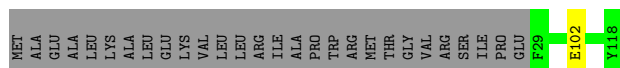
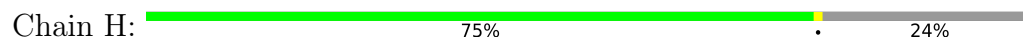
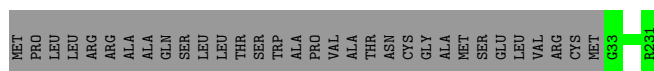
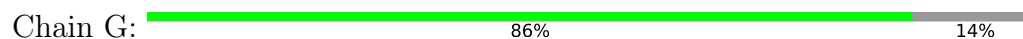
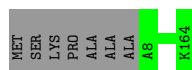
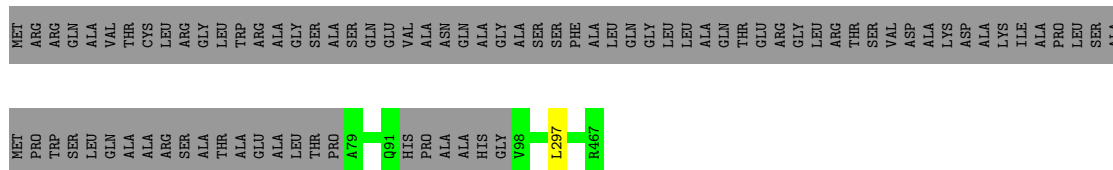
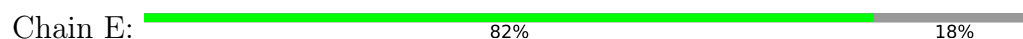
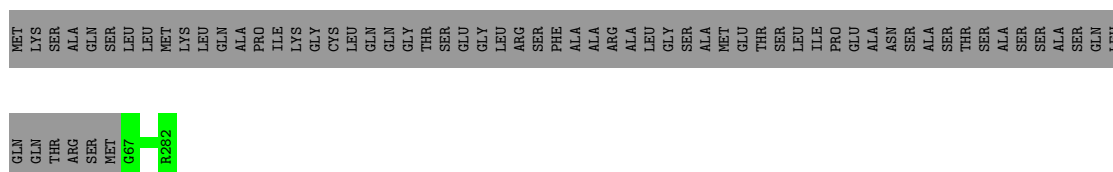
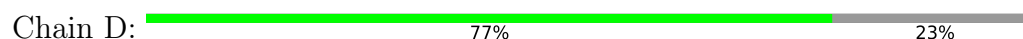
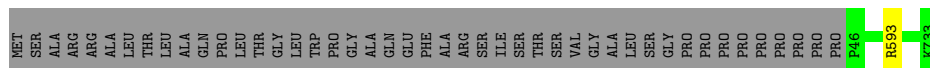
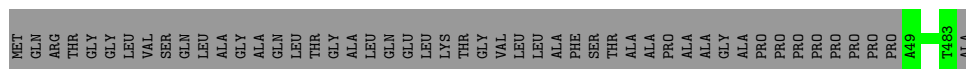
- Molecule 23: NADH:ubiquinone oxidoreductase 24 kD subunit

Chain A: 85% 15%




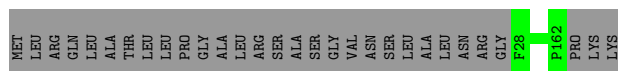
- Molecule 24: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial

Chain B: 90% 10%



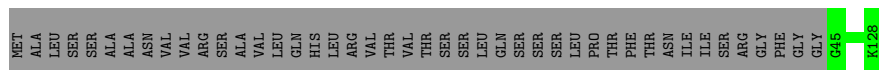
- Molecule 31: Mitochondrial NADH:ubiquinone oxidoreductase 18 kDa subunit

Chain I:  82% 18%



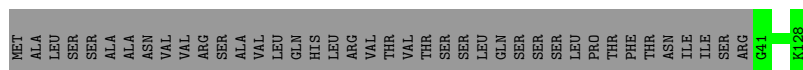
- Molecule 32: Acyl carrier protein

Chain J:  66% 34%




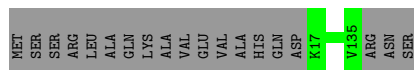
- Molecule 32: Acyl carrier protein

Chain r:  69% 31%




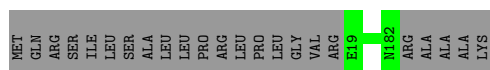
- Molecule 33: NADH:ubiquinone oxidoreductase B14 subunit

Chain K:  86% 14%




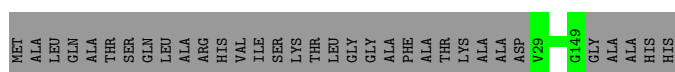
- Molecule 34: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

Chain L:  88% 12%



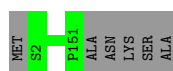
- Molecule 35: NADH:ubiquinone oxidoreductase 13 kD-like subunit

Chain M:  79% 21%

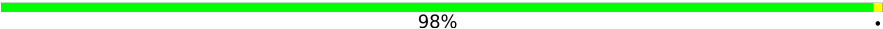


- Molecule 36: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

Chain N:  96%



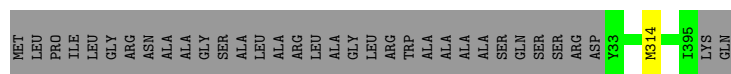
- Molecule 37: NADH:ubiquinone oxidoreductase B8 subunit

Chain O:  98% ..



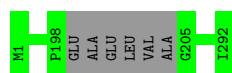
- Molecule 38: Putative NADH:ubiquinone oxidoreductase 39 kDa subunit

Chain P:  91% 9%



- Molecule 39: NADH-ubiquinone oxidoreductase chain 1

Chain Q:  98% .



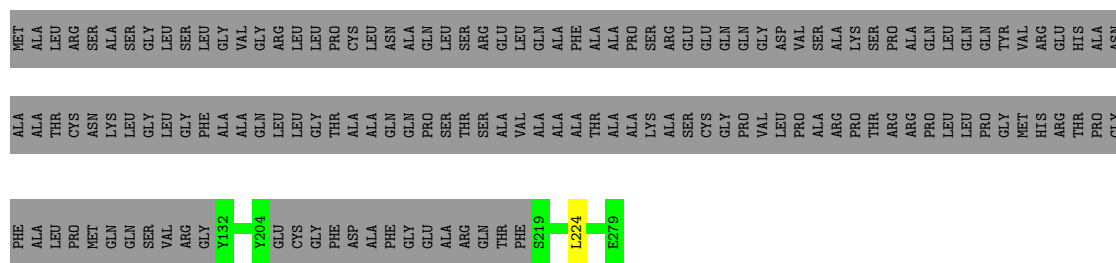
- Molecule 40: NADH-ubiquinone oxidoreductase chain 2

Chain R:  100%

There are no outlier residues recorded for this chain.

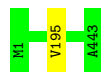
- Molecule 41: NADH-ubiquinone oxidoreductase chain 3

Chain S:  48% 52%



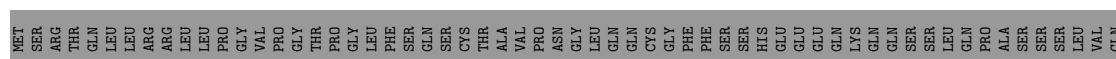
- Molecule 42: NADH-ubiquinone oxidoreductase chain 4

Chain T:  100%



- Molecule 43: NADH dehydrogenase subunit 4L

Chain U:  46% 54%





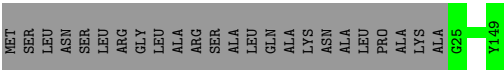
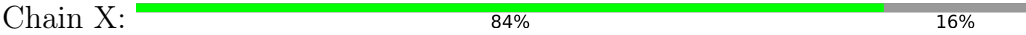
• Molecule 44: NADH-ubiquinone oxidoreductase chain 5



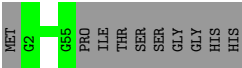
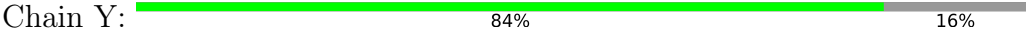
• Molecule 45: NADH-ubiquinone oxidoreductase chain 6



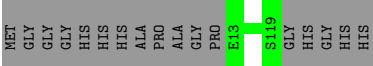
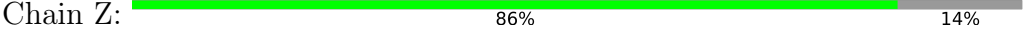
• Molecule 46: ASHI



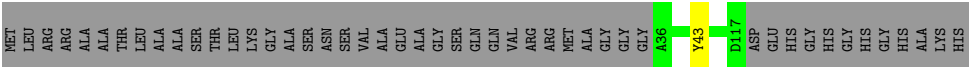
• Molecule 47: P9



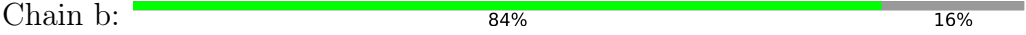
• Molecule 48: KFYI

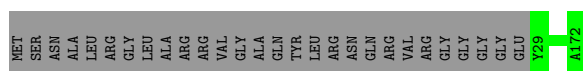


• Molecule 49: AGGG



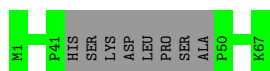
• Molecule 50: ESSS





- Molecule 51: B9

Chain c: 88% 12%



- Molecule 52: Mitochondrial NADH:ubiquinone oxidoreductase 10 kDa subunit

Chain d: 99%



- Molecule 53: Mitochondrial NADH:ubiquinone oxidoreductase 23 kDa subunit

Chain e: 99%



- Molecule 54: Mitochondrial NADH:ubiquinone oxidoreductase 7.5 kDa subunit

Chain f: 98%



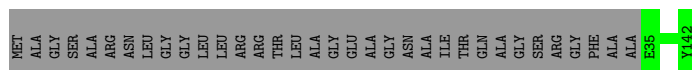
- Molecule 55: Mitochondrial putative NADH:ubiquinone oxidoreductase 6.5 kDa subunit

Chain g: 91% 9%



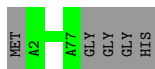
- Molecule 56: Mitochondrial NADH:ubiquinone oxidoreductase 13 kDa subunit

Chain h: 76% 24%



- Molecule 57: NADH:ubiquinone oxidoreductase 15 kDa subunit-like

Chain i: 94% 6%



- Molecule 58: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7

Chain j: 99%



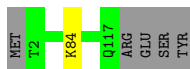
- Molecule 59: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

Chain k: 100%

There are no outlier residues recorded for this chain.

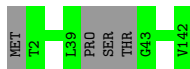
- Molecule 60: NADH:ubiquinone oxidoreductase 20,9 kD-like subunit

Chain l: 95%



- Molecule 61: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Chain m: 97%



- Molecule 62: Putative NADH:ubiquinone oxidoreductase 12.5 kDa subunit

Chain n: 98%



- Molecule 63: Putative NADH:ubiquinone oxidoreductase 17.8 kDa subunit

Chain o: 98%



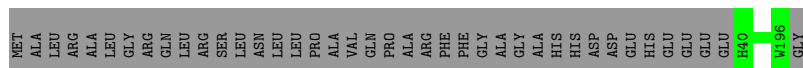
- Molecule 64: Mitochondrial NADH:ubiquinone oxidoreductase 16 kDa subunit

Chain p: 99%



- Molecule 65: Mitochondrial NADH:ubiquinone oxidoreductase 19 kDa subunit

Chain q: 80% 20%



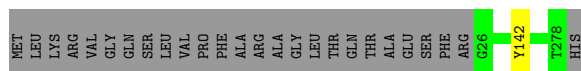
- Molecule 66: Mitochondrial NADH:ubiquinone oxidoreductase 32 kDa subunit

Chain s: 100%



- Molecule 67: CAG2 - CA-like

Chain t: 90% 9%



- Molecule 68: CAG1

Chain u: 100%



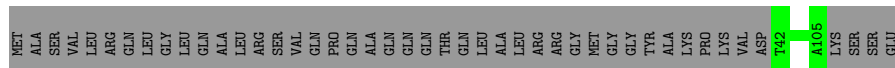
- Molecule 69: P10

Chain v: 100%

There are no outlier residues recorded for this chain.

- Molecule 70: Mitochondrial NADH:ubiquinone oxidoreductase 9 kDa subunit

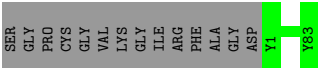
Chain w: 59% 41%



- Molecule 71: NUOP8

Chain x: 53% 47%





● Molecule 72: NUOP7



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83443	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, HEM, CDL, PC7, PTY, SF4, ZN, CU, FMN, FES, HEC, HEA, 3PH, CUA, NDP, UQ5, 8Q1, PGT, COO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1A	0.34	0/3060	0.52	1/4187 (0.0%)
1	1B	0.35	0/3060	0.53	0/4187
2	1C	0.28	0/1643	0.50	0/2233
2	1D	0.28	0/1643	0.50	0/2233
3	1E	0.34	0/1953	0.53	1/2654 (0.0%)
3	1F	0.33	0/1953	0.52	0/2654
4	1G	0.32	0/496	0.54	0/667
4	1H	0.32	0/496	0.50	0/667
5	1I	0.31	0/567	0.50	0/766
5	1J	0.30	0/567	0.45	0/766
6	1K	0.33	0/609	0.54	0/817
6	1L	0.31	0/609	0.54	0/817
7	1M	0.31	0/3723	0.54	0/5046
7	1N	0.30	0/3723	0.54	0/5046
8	1O	0.28	0/385	0.53	0/531
8	1P	0.29	0/385	0.59	0/531
9	1Q	0.31	0/3258	0.54	0/4439
9	1S	0.30	0/3258	0.53	0/4439
10	1R	0.31	0/996	0.55	0/1349
10	1T	0.33	0/996	0.57	0/1349
11	2A	0.33	0/4011	0.54	1/5484 (0.0%)
11	3A	0.34	0/4011	0.56	1/5484 (0.0%)
12	2B	0.30	0/1204	0.51	0/1641
12	3B	0.30	0/1204	0.52	0/1641
13	2C	0.30	0/1237	0.53	0/1676
13	3C	0.32	0/1237	0.55	0/1676
14	2D	0.32	0/2152	0.49	0/2937
14	3D	0.32	0/2152	0.50	0/2937
15	2E	0.31	0/757	0.63	0/1029
15	3E	0.32	0/757	0.60	0/1029
16	2F	0.30	0/726	0.46	0/974

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	3F	0.30	0/726	0.46	0/974
17	2G	0.30	0/762	0.58	1/1038 (0.1%)
17	3G	0.30	0/762	0.55	1/1038 (0.1%)
18	2H	0.30	0/980	0.51	0/1325
18	3H	0.32	0/980	0.55	0/1325
19	2I	0.33	0/619	0.51	0/839
19	3I	0.31	0/619	0.50	0/839
20	2J	0.30	0/839	0.51	0/1143
20	3J	0.31	0/839	0.53	0/1143
21	2K	0.31	0/392	0.51	0/531
21	3K	0.32	0/392	0.51	0/531
22	2L	0.31	0/621	0.56	0/841
22	3L	0.30	0/645	0.55	0/875
23	A	0.31	0/1878	0.54	0/2549
24	B	0.33	0/3400	0.56	0/4573
25	C	0.31	0/5272	0.56	0/7143
26	D	0.36	0/1843	0.58	0/2506
27	E	0.38	0/3158	0.61	1/4270 (0.0%)
28	F	0.41	0/1258	0.57	0/1706
29	G	0.32	0/1648	0.60	0/2222
30	H	0.35	0/773	0.60	1/1046 (0.1%)
31	I	0.31	0/1061	0.49	0/1441
32	J	0.29	0/649	0.49	0/875
32	r	0.32	0/673	0.47	0/906
33	K	0.34	0/1007	0.59	0/1348
34	L	0.33	0/1306	0.59	0/1769
35	M	0.31	0/936	0.52	0/1276
36	N	0.32	0/1277	0.52	0/1735
37	O	0.28	0/772	0.60	1/1037 (0.1%)
38	P	0.30	0/2879	0.55	1/3905 (0.0%)
39	Q	0.36	0/2234	0.58	0/3034
40	R	0.36	0/3100	0.55	0/4226
41	S	0.37	0/1106	0.57	1/1512 (0.1%)
42	T	0.37	1/3533 (0.0%)	0.56	0/4825
43	U	0.34	0/819	0.53	0/1112
44	V	0.36	0/4258	0.57	2/5792 (0.0%)
45	W	0.34	0/1239	0.52	0/1686
46	X	0.36	0/1081	0.55	0/1479
47	Y	0.32	0/411	0.49	0/557
48	Z	0.33	0/894	0.53	0/1218
49	a	0.33	0/698	0.47	0/949
50	b	0.35	0/1201	0.56	0/1623
51	c	0.31	0/463	0.53	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
52	d	0.37	0/721	0.53	0/968
53	e	0.34	0/1688	0.54	0/2301
54	f	0.32	0/547	0.53	0/740
55	g	0.30	0/433	0.55	0/587
56	h	0.34	0/948	0.55	0/1285
57	i	0.32	0/644	0.60	0/860
58	j	0.34	0/732	0.54	0/983
59	k	0.32	0/1011	0.55	0/1361
60	l	0.33	0/936	0.49	0/1278
61	m	0.36	0/1155	0.56	0/1558
62	n	0.32	0/886	0.50	0/1188
63	o	0.33	0/1265	0.59	0/1705
64	p	0.32	0/1095	0.55	0/1480
65	q	0.32	0/1308	0.51	0/1779
66	s	0.32	0/2353	0.53	1/3202 (0.0%)
67	t	0.32	0/2043	0.56	0/2778
68	u	0.32	0/1730	0.54	0/2341
69	v	0.33	0/369	0.48	0/498
70	w	0.34	0/521	0.49	0/702
71	x	0.34	0/727	0.49	0/994
72	y	0.34	0/963	0.52	0/1313
All	All	0.33	1/134906 (0.0%)	0.54	14/183172 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1A	0	1
1	1B	0	1
17	3G	0	1
53	e	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	T	195	VAL	CB-CG1	-5.47	1.41	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	O	7	LEU	CA-CB-CG	7.19	131.83	115.30
27	E	297	LEU	CA-CB-CG	6.98	131.35	115.30
17	2G	74	LEU	CA-CB-CG	6.55	130.36	115.30
17	3G	74	LEU	CA-CB-CG	6.43	130.10	115.30
11	3A	417	LEU	CA-CB-CG	6.25	129.68	115.30
41	S	224	LEU	CA-CB-CG	6.21	129.59	115.30
66	s	94	LEU	CA-CB-CG	5.91	128.90	115.30
44	V	8	PHE	CB-CG-CD1	-5.81	116.73	120.80
38	P	314	MET	CA-CB-CG	5.76	123.09	113.30
30	H	102	GLU	C-N-CA	5.64	135.79	121.70
11	2A	417	LEU	CA-CB-CG	5.63	128.25	115.30
3	1E	110	CYS	CA-CB-SG	5.16	123.30	114.00
44	V	8	PHE	CB-CG-CD2	5.12	124.38	120.80
1	1A	150	LEU	CA-CB-CG	5.06	126.93	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1A	184	TYR	Sidechain
1	1B	184	TYR	Sidechain
17	3G	114	TRP	Peptide
53	e	147	MET	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1A	374/381 (98%)	363 (97%)	11 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1B	374/381 (98%)	366 (98%)	8 (2%)	0	100	100
2	1C	205/262 (78%)	194 (95%)	11 (5%)	0	100	100
2	1D	205/262 (78%)	201 (98%)	4 (2%)	0	100	100
3	1E	241/314 (77%)	236 (98%)	5 (2%)	0	100	100
3	1F	241/314 (77%)	235 (98%)	6 (2%)	0	100	100
4	1G	57/60 (95%)	57 (100%)	0	0	100	100
4	1H	57/60 (95%)	57 (100%)	0	0	100	100
5	1I	66/69 (96%)	66 (100%)	0	0	100	100
5	1J	66/69 (96%)	64 (97%)	2 (3%)	0	100	100
6	1K	68/73 (93%)	67 (98%)	1 (2%)	0	100	100
6	1L	68/73 (93%)	65 (96%)	3 (4%)	0	100	100
7	1M	462/495 (93%)	454 (98%)	8 (2%)	0	100	100
7	1N	462/495 (93%)	456 (99%)	5 (1%)	1 (0%)	44	71
8	1O	46/59 (78%)	43 (94%)	3 (6%)	0	100	100
8	1P	46/59 (78%)	44 (96%)	2 (4%)	0	100	100
9	1Q	439/485 (90%)	418 (95%)	20 (5%)	1 (0%)	44	71
9	1S	439/485 (90%)	425 (97%)	12 (3%)	2 (0%)	25	54
10	1R	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
10	1T	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
11	2A	502/504 (100%)	489 (97%)	13 (3%)	0	100	100
11	3A	502/504 (100%)	490 (98%)	12 (2%)	0	100	100
12	2B	139/284 (49%)	136 (98%)	3 (2%)	0	100	100
12	3B	139/284 (49%)	135 (97%)	4 (3%)	0	100	100
13	2C	151/153 (99%)	144 (95%)	7 (5%)	0	100	100
13	3C	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
14	2D	264/382 (69%)	255 (97%)	9 (3%)	0	100	100
14	3D	264/382 (69%)	254 (96%)	10 (4%)	0	100	100
15	2E	88/175 (50%)	85 (97%)	2 (2%)	1 (1%)	12	35
15	3E	88/175 (50%)	85 (97%)	2 (2%)	1 (1%)	12	35
16	2F	84/96 (88%)	81 (96%)	3 (4%)	0	100	100
16	3F	84/96 (88%)	80 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	2G	87/125 (70%)	78 (90%)	9 (10%)	0	100	100
17	3G	87/125 (70%)	80 (92%)	7 (8%)	0	100	100
18	2H	112/148 (76%)	108 (96%)	4 (4%)	0	100	100
18	3H	112/148 (76%)	108 (96%)	4 (4%)	0	100	100
19	2I	70/101 (69%)	67 (96%)	3 (4%)	0	100	100
19	3I	70/101 (69%)	67 (96%)	3 (4%)	0	100	100
20	2J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
20	3J	102/105 (97%)	100 (98%)	2 (2%)	0	100	100
21	2K	45/58 (78%)	44 (98%)	1 (2%)	0	100	100
21	3K	45/58 (78%)	44 (98%)	1 (2%)	0	100	100
22	2L	74/87 (85%)	70 (95%)	4 (5%)	0	100	100
22	3L	76/87 (87%)	72 (95%)	4 (5%)	0	100	100
23	A	237/282 (84%)	228 (96%)	9 (4%)	0	100	100
24	B	433/484 (90%)	417 (96%)	16 (4%)	0	100	100
25	C	686/733 (94%)	667 (97%)	19 (3%)	0	100	100
26	D	214/282 (76%)	204 (95%)	10 (5%)	0	100	100
27	E	379/467 (81%)	368 (97%)	11 (3%)	0	100	100
28	F	155/164 (94%)	149 (96%)	6 (4%)	0	100	100
29	G	197/231 (85%)	189 (96%)	8 (4%)	0	100	100
30	H	88/118 (75%)	81 (92%)	7 (8%)	0	100	100
31	I	133/165 (81%)	130 (98%)	3 (2%)	0	100	100
32	J	82/128 (64%)	76 (93%)	6 (7%)	0	100	100
32	r	86/128 (67%)	84 (98%)	2 (2%)	0	100	100
33	K	117/138 (85%)	115 (98%)	2 (2%)	0	100	100
34	L	162/187 (87%)	155 (96%)	7 (4%)	0	100	100
35	M	119/154 (77%)	111 (93%)	8 (7%)	0	100	100
36	N	148/156 (95%)	145 (98%)	3 (2%)	0	100	100
37	O	98/101 (97%)	94 (96%)	4 (4%)	0	100	100
38	P	361/397 (91%)	350 (97%)	11 (3%)	0	100	100
39	Q	282/292 (97%)	274 (97%)	8 (3%)	0	100	100
40	R	385/387 (100%)	369 (96%)	16 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	S	130/279 (47%)	128 (98%)	2 (2%)	0	100	100
42	T	441/443 (100%)	431 (98%)	10 (2%)	0	100	100
43	U	103/227 (45%)	102 (99%)	1 (1%)	0	100	100
44	V	544/546 (100%)	525 (96%)	18 (3%)	1 (0%)	44	71
45	W	155/162 (96%)	151 (97%)	4 (3%)	0	100	100
46	X	123/149 (83%)	117 (95%)	6 (5%)	0	100	100
47	Y	52/64 (81%)	52 (100%)	0	0	100	100
48	Z	105/124 (85%)	100 (95%)	5 (5%)	0	100	100
49	a	80/129 (62%)	78 (98%)	1 (1%)	1 (1%)	10	30
50	b	142/172 (83%)	139 (98%)	3 (2%)	0	100	100
51	c	55/67 (82%)	52 (94%)	3 (6%)	0	100	100
52	d	83/86 (96%)	82 (99%)	1 (1%)	0	100	100
53	e	216/219 (99%)	214 (99%)	1 (0%)	1 (0%)	25	54
54	f	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
55	g	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
56	h	106/142 (75%)	97 (92%)	9 (8%)	0	100	100
57	i	74/81 (91%)	73 (99%)	1 (1%)	0	100	100
58	j	83/86 (96%)	80 (96%)	3 (4%)	0	100	100
59	k	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
60	l	114/121 (94%)	110 (96%)	4 (4%)	0	100	100
61	m	134/142 (94%)	133 (99%)	1 (1%)	0	100	100
62	n	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
63	o	150/155 (97%)	145 (97%)	5 (3%)	0	100	100
64	p	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
65	q	155/197 (79%)	149 (96%)	6 (4%)	0	100	100
66	s	310/312 (99%)	303 (98%)	7 (2%)	0	100	100
67	t	251/279 (90%)	243 (97%)	8 (3%)	0	100	100
68	u	226/229 (99%)	220 (97%)	6 (3%)	0	100	100
69	v	43/45 (96%)	43 (100%)	0	0	100	100
70	w	62/109 (57%)	61 (98%)	1 (2%)	0	100	100
71	x	81/157 (52%)	81 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	y	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
All	All	16540/19385 (85%)	16027 (97%)	504 (3%)	9 (0%)	50	76

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	1Q	396	ASP
15	2E	28	TRP
15	3E	28	TRP
49	a	43	TYR
9	1S	66	THR
44	V	519	PRO
53	e	148	PRO
7	1N	187	VAL
9	1S	475	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1A	312/317 (98%)	311 (100%)	1 (0%)	91	97
1	1B	312/317 (98%)	309 (99%)	3 (1%)	73	91
2	1C	171/213 (80%)	170 (99%)	1 (1%)	84	94
2	1D	171/213 (80%)	171 (100%)	0	100	100
3	1E	191/238 (80%)	191 (100%)	0	100	100
3	1F	191/238 (80%)	191 (100%)	0	100	100
4	1G	52/53 (98%)	52 (100%)	0	100	100
4	1H	52/53 (98%)	52 (100%)	0	100	100
5	1I	58/59 (98%)	58 (100%)	0	100	100
5	1J	58/59 (98%)	58 (100%)	0	100	100
6	1K	62/64 (97%)	62 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	1L	62/64 (97%)	62 (100%)	0	100	100
7	1M	390/413 (94%)	390 (100%)	0	100	100
7	1N	390/413 (94%)	388 (100%)	2 (0%)	86	95
8	1O	38/47 (81%)	38 (100%)	0	100	100
8	1P	38/47 (81%)	38 (100%)	0	100	100
9	1Q	333/362 (92%)	331 (99%)	2 (1%)	84	94
9	1S	333/362 (92%)	332 (100%)	1 (0%)	91	97
10	1R	106/107 (99%)	106 (100%)	0	100	100
10	1T	106/107 (99%)	106 (100%)	0	100	100
11	2A	408/408 (100%)	408 (100%)	0	100	100
11	3A	408/408 (100%)	408 (100%)	0	100	100
12	2B	132/224 (59%)	132 (100%)	0	100	100
12	3B	132/224 (59%)	132 (100%)	0	100	100
13	2C	137/137 (100%)	137 (100%)	0	100	100
13	3C	137/137 (100%)	137 (100%)	0	100	100
14	2D	211/294 (72%)	211 (100%)	0	100	100
14	3D	211/294 (72%)	211 (100%)	0	100	100
15	2E	79/137 (58%)	79 (100%)	0	100	100
15	3E	79/137 (58%)	79 (100%)	0	100	100
16	2F	66/72 (92%)	66 (100%)	0	100	100
16	3F	66/72 (92%)	66 (100%)	0	100	100
17	2G	75/100 (75%)	75 (100%)	0	100	100
17	3G	75/100 (75%)	74 (99%)	1 (1%)	65	88
18	2H	103/132 (78%)	103 (100%)	0	100	100
18	3H	103/132 (78%)	103 (100%)	0	100	100
19	2I	58/80 (72%)	58 (100%)	0	100	100
19	3I	58/80 (72%)	58 (100%)	0	100	100
20	2J	83/84 (99%)	83 (100%)	0	100	100
20	3J	83/84 (99%)	83 (100%)	0	100	100
21	2K	39/46 (85%)	39 (100%)	0	100	100
21	3K	39/46 (85%)	39 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	2L	63/74 (85%)	63 (100%)	0	100	100
22	3L	65/74 (88%)	65 (100%)	0	100	100
23	A	197/228 (86%)	197 (100%)	0	100	100
24	B	344/377 (91%)	344 (100%)	0	100	100
25	C	537/572 (94%)	536 (100%)	1 (0%)	92	97
26	D	196/248 (79%)	196 (100%)	0	100	100
27	E	329/388 (85%)	329 (100%)	0	100	100
28	F	129/133 (97%)	129 (100%)	0	100	100
29	G	172/198 (87%)	172 (100%)	0	100	100
30	H	82/105 (78%)	82 (100%)	0	100	100
31	I	111/134 (83%)	111 (100%)	0	100	100
32	J	71/108 (66%)	71 (100%)	0	100	100
32	r	72/108 (67%)	72 (100%)	0	100	100
33	K	106/122 (87%)	106 (100%)	0	100	100
34	L	130/148 (88%)	130 (100%)	0	100	100
35	M	100/121 (83%)	100 (100%)	0	100	100
36	N	128/132 (97%)	128 (100%)	0	100	100
37	O	80/81 (99%)	80 (100%)	0	100	100
38	P	305/327 (93%)	305 (100%)	0	100	100
39	Q	230/234 (98%)	230 (100%)	0	100	100
40	R	321/321 (100%)	321 (100%)	0	100	100
41	S	111/217 (51%)	111 (100%)	0	100	100
42	T	374/374 (100%)	374 (100%)	0	100	100
43	U	84/180 (47%)	84 (100%)	0	100	100
44	V	439/439 (100%)	439 (100%)	0	100	100
45	W	131/135 (97%)	131 (100%)	0	100	100
46	X	105/122 (86%)	105 (100%)	0	100	100
47	Y	38/46 (83%)	38 (100%)	0	100	100
48	Z	93/102 (91%)	93 (100%)	0	100	100
49	a	68/98 (69%)	68 (100%)	0	100	100
50	b	119/138 (86%)	119 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	c	49/56 (88%)	49 (100%)	0	100	100
52	d	63/64 (98%)	63 (100%)	0	100	100
53	e	163/164 (99%)	163 (100%)	0	100	100
54	f	52/53 (98%)	52 (100%)	0	100	100
55	g	40/45 (89%)	40 (100%)	0	100	100
56	h	91/110 (83%)	91 (100%)	0	100	100
57	i	65/67 (97%)	65 (100%)	0	100	100
58	j	72/73 (99%)	72 (100%)	0	100	100
59	k	102/102 (100%)	102 (100%)	0	100	100
60	l	94/99 (95%)	93 (99%)	1 (1%)	70	90
61	m	118/122 (97%)	118 (100%)	0	100	100
62	n	92/94 (98%)	92 (100%)	0	100	100
63	o	130/132 (98%)	130 (100%)	0	100	100
64	p	109/110 (99%)	109 (100%)	0	100	100
65	q	135/165 (82%)	135 (100%)	0	100	100
66	s	243/243 (100%)	243 (100%)	0	100	100
67	t	212/233 (91%)	211 (100%)	1 (0%)	86	95
68	u	180/181 (99%)	180 (100%)	0	100	100
69	v	38/38 (100%)	38 (100%)	0	100	100
70	w	55/91 (60%)	55 (100%)	0	100	100
71	x	70/130 (54%)	70 (100%)	0	100	100
72	y	102/106 (96%)	102 (100%)	0	100	100
All	All	13813/15736 (88%)	13799 (100%)	14 (0%)	92	98

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1A	316	ARG
1	1B	79	ARG
1	1B	261	ASN
1	1B	316	ARG
2	1C	230	HIS
7	1N	171	ARG
7	1N	488	ARG

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Mol	Chain	Res	Type
9	1Q	81	ARG
9	1Q	483	ARG
9	1S	216	ARG
17	3G	109	ARG
25	C	593	ARG
60	l	84	LYS
67	t	142	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	1B	261	ASN
25	C	279	ASN
25	C	297	ASN
25	C	618	GLN
60	l	41	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 107 ligands modelled in this entry, 7 are monoatomic - leaving 100 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
88	SF4	C	803	25	0,12,12	-	-	-		
74	HEM	1A	403	1	41,50,50	1.42	4 (9%)	45,82,82	1.76	11 (24%)
81	PGT	T	502	-	47,47,50	0.53	0	50,53,56	0.56	1 (2%)
77	PTY	1E	403	-	33,33,49	0.55	0	36,38,54	0.50	0
77	PTY	T	501	-	49,49,49	0.46	0	52,54,54	0.62	1 (1%)
79	PC7	2A	606	-	26,26,51	0.66	0	32,34,59	0.70	0
77	PTY	T	504	-	27,27,49	0.65	0	30,32,54	0.48	0
82	HEA	3A	602	11	57,67,67	2.05	16 (28%)	61,103,103	2.43	25 (40%)
81	PGT	2A	601	-	32,32,50	0.61	0	35,38,56	0.60	0
79	PC7	T	503	-	51,51,51	0.50	0	57,59,59	0.59	0
79	PC7	1H	101	-	38,38,51	0.57	0	44,46,59	0.56	0
76	3PH	R	401	-	31,31,47	0.75	1 (3%)	35,36,52	0.73	2 (5%)
76	3PH	1A	406	-	30,30,47	0.78	1 (3%)	34,35,52	0.69	1 (2%)
77	PTY	V	604	-	39,39,49	0.54	0	42,44,54	0.50	0
77	PTY	V	605	-	49,49,49	0.46	0	52,54,54	0.38	0
82	HEA	2A	602	11	57,67,67	2.06	17 (29%)	61,103,103	2.43	25 (40%)
86	FES	C	801	25	0,4,4	-	-	-		
79	PC7	3A	606	-	26,26,51	0.66	0	32,34,59	0.65	0
86	FES	A	301	23	0,4,4	-	-	-		
76	3PH	y	201	-	31,31,47	0.78	1 (3%)	35,36,52	0.66	1 (2%)
81	PGT	3A	601	-	32,32,50	0.59	0	35,38,56	0.52	0
78	HEC	1E	404	3	32,50,50	2.19	3 (9%)	24,82,82	1.81	5 (20%)
75	CDL	1K	101	-	78,78,99	0.43	0	84,90,111	0.28	0
76	3PH	1R	201	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
79	PC7	u	601	-	41,41,51	0.55	0	47,49,59	0.68	2 (4%)
77	PTY	G	303	-	42,42,49	0.49	0	45,47,54	0.44	0
75	CDL	R	405	-	62,62,99	0.40	0	68,74,111	0.28	0
75	CDL	y	202	-	54,54,99	0.53	1 (1%)	60,66,111	0.32	0
75	CDL	x	101	-	91,91,99	0.40	1 (1%)	97,103,111	0.24	0
73	UQ5	1A	401	-	38,38,38	0.53	0	46,49,49	1.08	4 (8%)
89	8Q1	r	200	-	31,34,34	1.76	5 (16%)	40,43,43	1.88	10 (25%)
75	CDL	W	701	-	94,94,99	0.35	0	100,106,111	0.28	0
77	PTY	e	302	-	42,42,49	0.52	0	45,47,54	0.42	0
73	UQ5	1B	401	-	38,38,38	0.46	0	46,49,49	0.73	1 (2%)
76	3PH	h	201	-	44,44,47	0.65	1 (2%)	48,49,52	3.77	5 (10%)
76	3PH	V	601	-	41,41,47	0.66	1 (2%)	45,46,52	0.63	1 (2%)
75	CDL	1A	405	-	58,58,99	0.44	0	64,70,111	0.27	0
77	PTY	2D	301	-	34,34,49	0.56	0	37,39,54	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
75	CDL	1M	501	-	53,53,99	0.49	1 (1%)	59,65,111	0.26	0
75	CDL	1B	408	-	70,70,99	0.34	0	76,82,111	0.34	0
77	PTY	x	102	-	49,49,49	0.46	0	52,54,54	0.40	0
77	PTY	R	404	-	43,43,49	0.51	0	46,48,54	0.46	0
75	CDL	1B	405	-	63,63,99	0.44	1 (1%)	69,75,111	0.25	0
82	HEA	2A	603	11	57,67,67	2.08	16 (28%)	61,103,103	2.42	23 (37%)
75	CDL	V	603	-	63,63,99	0.41	0	69,75,111	0.25	0
73	UQ5	1B	402	-	38,38,38	0.51	0	46,49,49	1.51	6 (13%)
76	3PH	2D	302	-	31,31,47	0.77	1 (3%)	35,36,52	0.72	1 (2%)
75	CDL	u	602	-	82,82,99	0.38	0	88,94,111	0.30	0
75	CDL	1L	101	-	58,58,99	0.43	0	64,70,111	0.35	0
77	PTY	S	302	-	45,45,49	0.49	0	48,50,54	0.41	0
76	3PH	w	201	-	44,44,47	0.64	1 (2%)	48,49,52	0.75	3 (6%)
90	NDP	P	401	-	45,52,52	2.24	6 (13%)	53,80,80	1.65	13 (24%)
74	HEM	1B	404	1	41,50,50	1.45	3 (7%)	45,82,82	1.38	7 (15%)
76	3PH	1B	406	-	47,47,47	0.62	1 (2%)	51,52,52	0.60	1 (1%)
85	CUA	3C	301	-	0,1,1	-	-	-	-	-
77	PTY	T	506	-	25,25,49	0.64	0	28,30,54	0.47	0
77	PTY	2F	101	-	33,33,49	0.55	0	36,38,54	0.45	0
77	PTY	e	301	-	24,24,49	0.64	0	27,29,54	0.52	0
91	COO	s	401	-	45,55,55	0.82	1 (2%)	55,81,81	4.26	10 (18%)
76	3PH	1E	402	-	39,39,47	0.69	1 (2%)	43,44,52	0.64	0
88	SF4	B	502	24	0,12,12	-	-	-	-	-
85	CUA	2C	301	-	0,1,1	-	-	-	-	-
73	UQ5	Q	301	-	38,38,38	0.51	0	46,49,49	0.83	3 (6%)
76	3PH	3D	302	-	31,31,47	0.75	1 (3%)	35,36,52	0.80	1 (2%)
74	HEM	1B	403	1	41,50,50	1.54	4 (9%)	45,82,82	1.51	7 (15%)
77	PTY	h	202	-	45,45,49	0.47	0	48,50,54	0.46	0
82	HEA	3A	603	11	57,67,67	2.06	15 (26%)	61,103,103	2.46	23 (37%)
88	SF4	G	302	29	0,12,12	-	-	-	-	-
77	PTY	V	606	-	34,34,49	0.56	0	37,39,54	0.44	0
87	FMN	B	501	-	33,33,33	1.09	2 (6%)	48,50,50	1.25	8 (16%)
79	PC7	R	403	-	43,43,51	0.53	0	49,51,59	0.61	0
81	PGT	T	505	-	39,39,50	0.54	0	42,45,56	0.50	0
77	PTY	R	402	-	33,33,49	0.53	0	36,38,54	0.43	0
88	SF4	G	301	29	0,12,12	-	-	-	-	-
77	PTY	3D	301	-	34,34,49	0.57	0	37,39,54	0.47	0
76	3PH	2I	201	-	41,41,47	0.67	1 (2%)	45,46,52	0.67	1 (2%)
75	CDL	u	603	-	70,70,99	0.43	0	76,82,111	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
77	PTY	1F	403	-	37,37,49	0.51	0	40,42,54	0.44	0
88	SF4	C	802	25	0,12,12	-	-	-		
76	3PH	1B	407	-	47,47,47	0.63	1 (2%)	51,52,52	0.60	0
79	PC7	1G	301	-	35,35,51	0.61	0	41,43,59	0.60	1 (2%)
81	PGT	l	701	-	50,50,50	0.48	0	53,56,56	0.59	1 (1%)
76	3PH	3I	201	-	41,41,47	0.65	1 (2%)	45,46,52	0.66	1 (2%)
76	3PH	S	301	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
76	3PH	c	101	-	47,47,47	0.62	1 (2%)	51,52,52	0.63	1 (1%)
75	CDL	1E	401	-	52,52,99	0.44	0	58,64,111	0.25	0
81	PGT	b	601	-	43,43,50	0.53	0	46,49,56	0.51	0
88	SF4	F	201	28	0,12,12	-	-	-		
75	CDL	h	203	-	76,76,99	0.37	0	82,88,111	0.25	0
73	UQ5	1A	402	-	38,38,38	0.52	0	46,49,49	0.66	1 (2%)
78	HEC	1F	402	3	32,50,50	2.08	3 (9%)	24,82,82	1.85	6 (25%)
76	3PH	V	602	-	40,40,47	0.67	1 (2%)	44,45,52	0.82	1 (2%)
74	HEM	1A	404	1	41,50,50	1.40	3 (7%)	45,82,82	1.52	7 (15%)
79	PC7	Q	302	-	32,32,51	0.59	0	38,40,59	0.69	0
76	3PH	g	101	-	36,36,47	0.71	1 (2%)	40,41,52	0.70	1 (2%)
77	PTY	R	406	-	39,39,49	0.53	0	42,44,54	0.51	0
89	8Q1	J	200	-	31,34,34	1.69	5 (16%)	40,43,43	1.71	5 (12%)
77	PTY	3F	101	-	33,33,49	0.55	0	36,38,54	0.47	0
75	CDL	1F	401	-	55,55,99	0.42	0	61,67,111	0.27	0
76	3PH	1K	102	-	47,47,47	0.64	1 (2%)	51,52,52	0.60	2 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
88	SF4	C	803	25	-	-	0/6/5/5
74	HEM	1A	403	1	-	3/12/54/54	-
81	PGT	T	502	-	-	20/52/52/55	-
77	PTY	1E	403	-	-	15/37/37/53	-
77	PTY	T	501	-	-	19/53/53/53	-
79	PC7	2A	606	-	-	10/30/30/55	-
77	PTY	T	504	-	-	11/31/31/53	-
82	HEA	3A	602	11	-	7/32/76/76	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	PGT	2A	601	-	-	10/37/37/55	-
79	PC7	T	503	-	-	22/55/55/55	-
79	PC7	1H	101	-	-	19/42/42/55	-
76	3PH	R	401	-	-	13/33/33/49	-
76	3PH	1A	406	-	-	13/32/32/49	-
77	PTY	V	604	-	-	15/43/43/53	-
77	PTY	V	605	-	-	25/53/53/53	-
82	HEA	2A	602	11	-	7/32/76/76	-
86	FES	C	801	25	-	-	0/1/1/1
79	PC7	3A	606	-	-	22/30/30/55	-
86	FES	A	301	23	-	-	0/1/1/1
76	3PH	y	201	-	-	13/33/33/49	-
81	PGT	3A	601	-	-	12/37/37/55	-
78	HEC	1E	404	3	-	0/10/54/54	-
75	CDL	1K	101	-	-	59/89/89/110	-
76	3PH	1R	201	-	-	13/38/38/49	-
79	PC7	u	601	-	-	15/45/45/55	-
77	PTY	G	303	-	-	6/46/46/53	-
75	CDL	R	405	-	-	43/73/73/110	-
75	CDL	y	202	-	-	30/65/65/110	-
75	CDL	x	101	-	-	65/102/102/110	-
73	UQ5	1A	401	-	-	10/33/57/57	0/1/1/1
89	8Q1	r	200	-	-	19/41/41/41	-
75	CDL	W	701	-	-	62/105/105/110	-
77	PTY	e	302	-	-	22/46/46/53	-
73	UQ5	1B	401	-	-	7/33/57/57	0/1/1/1
76	3PH	h	201	-	-	19/46/46/49	-
76	3PH	V	601	-	-	18/43/43/49	-
75	CDL	1A	405	-	-	34/69/69/110	-
77	PTY	2D	301	-	-	13/38/38/53	-
75	CDL	1M	501	-	-	31/64/64/110	-
75	CDL	1B	408	-	-	45/81/81/110	-
77	PTY	x	102	-	-	18/53/53/53	-
77	PTY	R	404	-	-	21/47/47/53	-
75	CDL	1B	405	-	-	49/74/74/110	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	HEA	2A	603	11	-	5/32/76/76	-
75	CDL	V	603	-	-	42/74/74/110	-
73	UQ5	1B	402	-	-	10/33/57/57	0/1/1/1
76	3PH	2D	302	-	-	19/33/33/49	-
75	CDL	u	602	-	-	51/93/93/110	-
75	CDL	1L	101	-	-	43/69/69/110	-
77	PTY	S	302	-	-	21/49/49/53	-
76	3PH	w	201	-	-	21/46/46/49	-
90	NDP	P	401	-	-	11/30/77/77	0/5/5/5
74	HEM	1B	404	1	-	4/12/54/54	-
76	3PH	1B	406	-	-	22/49/49/49	-
77	PTY	T	506	-	-	15/29/29/53	-
77	PTY	2F	101	-	-	15/37/37/53	-
77	PTY	e	301	-	-	9/28/28/53	-
91	COO	s	401	-	-	22/50/70/70	0/3/3/3
76	3PH	1E	402	-	-	17/41/41/49	-
88	SF4	B	502	24	-	-	0/6/5/5
73	UQ5	Q	301	-	-	4/33/57/57	0/1/1/1
76	3PH	3D	302	-	-	10/33/33/49	-
74	HEM	1B	403	1	-	3/12/54/54	-
77	PTY	h	202	-	-	20/49/49/53	-
82	HEA	3A	603	11	-	4/32/76/76	-
88	SF4	G	302	29	-	-	0/6/5/5
77	PTY	V	606	-	-	18/38/38/53	-
87	FMN	B	501	-	-	4/18/18/18	0/3/3/3
79	PC7	R	403	-	-	15/47/47/55	-
81	PGT	T	505	-	-	18/44/44/55	-
77	PTY	R	402	-	-	11/37/37/53	-
88	SF4	G	301	29	-	-	0/6/5/5
77	PTY	3D	301	-	-	15/38/38/53	-
76	3PH	2I	201	-	-	14/43/43/49	-
75	CDL	u	603	-	-	57/81/81/110	-
77	PTY	1F	403	-	-	17/41/41/53	-
88	SF4	C	802	25	-	-	0/6/5/5
76	3PH	1B	407	-	-	18/49/49/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	PC7	1G	301	-	-	16/39/39/55	-
81	PGT	l	701	-	-	27/55/55/55	-
76	3PH	3I	201	-	-	9/43/43/49	-
76	3PH	S	301	-	-	13/38/38/49	-
76	3PH	c	101	-	-	13/49/49/49	-
75	CDL	1E	401	-	-	41/63/63/110	-
81	PGT	b	601	-	-	27/48/48/55	-
88	SF4	F	201	28	-	-	0/6/5/5
75	CDL	h	203	-	-	58/87/87/110	-
73	UQ5	1A	402	-	-	9/33/57/57	0/1/1/1
78	HEC	1F	402	3	-	0/10/54/54	-
76	3PH	V	602	-	-	17/42/42/49	-
74	HEM	1A	404	1	-	4/12/54/54	-
79	PC7	Q	302	-	-	14/36/36/55	-
76	3PH	g	101	-	-	10/38/38/49	-
77	PTY	R	406	-	-	15/43/43/53	-
89	8Q1	J	200	-	-	11/41/41/41	-
77	PTY	3F	101	-	-	10/37/37/53	-
75	CDL	1F	401	-	-	32/66/66/110	-
76	3PH	1K	102	-	-	15/49/49/49	-

All (126) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
90	P	401	NDP	P2B-O2B	12.34	1.82	1.59
78	1E	404	HEC	C3C-C2C	-6.90	1.33	1.40
78	1F	402	HEC	C3C-C2C	-6.31	1.34	1.40
78	1E	404	HEC	C2B-C3B	-6.05	1.34	1.40
89	r	200	8Q1	C34-N36	5.99	1.46	1.33
78	1F	402	HEC	C2B-C3B	-5.79	1.34	1.40
82	2A	603	HEA	C3B-C2B	5.65	1.47	1.34
89	J	200	8Q1	C34-N36	5.48	1.45	1.33
82	3A	603	HEA	C3B-C2B	5.46	1.47	1.34
82	2A	602	HEA	C3A-C2A	5.36	1.47	1.40
82	3A	602	HEA	C3B-C2B	5.34	1.46	1.34
78	1E	404	HEC	C3D-C2D	5.30	1.53	1.37
78	1F	402	HEC	C3D-C2D	5.24	1.53	1.37
89	r	200	8Q1	C39-N41	5.24	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
74	1B	403	HEM	C3C-C2C	-5.21	1.33	1.40
82	3A	603	HEA	C3C-C2C	5.15	1.47	1.40
89	J	200	8Q1	C39-N41	5.13	1.45	1.33
82	2A	602	HEA	C3B-C2B	5.11	1.46	1.34
82	2A	603	HEA	CHC-C4B	4.98	1.47	1.35
82	2A	603	HEA	C3D-C2D	4.96	1.47	1.36
82	3A	603	HEA	CHC-C4B	4.91	1.47	1.35
82	2A	602	HEA	C3D-C2D	4.88	1.47	1.36
82	3A	602	HEA	C3C-C2C	4.88	1.47	1.40
82	3A	602	HEA	CHC-C4B	4.88	1.47	1.35
82	3A	602	HEA	C3A-C2A	4.83	1.47	1.40
82	2A	602	HEA	CHD-C1D	4.83	1.47	1.35
82	3A	602	HEA	C3D-C2D	4.80	1.46	1.36
82	2A	603	HEA	C3C-C2C	4.79	1.47	1.40
82	2A	603	HEA	C3A-C2A	4.77	1.47	1.40
82	3A	602	HEA	CHD-C1D	4.75	1.47	1.35
82	3A	603	HEA	C3A-C2A	4.73	1.46	1.40
82	3A	603	HEA	C3D-C2D	4.68	1.46	1.36
82	2A	603	HEA	CHD-C1D	4.68	1.47	1.35
82	2A	602	HEA	CHC-C4B	4.68	1.47	1.35
82	2A	602	HEA	C3C-C2C	4.67	1.46	1.40
82	3A	603	HEA	CHD-C1D	4.63	1.46	1.35
90	P	401	NDP	PN-O5D	3.82	1.74	1.59
74	1B	404	HEM	C3C-CAC	3.76	1.55	1.47
74	1B	403	HEM	C3C-CAC	3.70	1.55	1.47
74	1A	404	HEM	C3C-CAC	3.70	1.55	1.47
74	1A	403	HEM	C3C-CAC	3.67	1.55	1.47
74	1B	404	HEM	C3C-C2C	-3.66	1.35	1.40
74	1A	403	HEM	C3C-C2C	-3.64	1.35	1.40
74	1A	404	HEM	C3C-C2C	-3.61	1.35	1.40
87	B	501	FMN	C4A-N5	3.60	1.37	1.30
76	y	201	3PH	P-O11	3.39	1.71	1.60
76	V	602	3PH	P-O11	3.38	1.71	1.60
76	1B	407	3PH	P-O11	3.36	1.71	1.60
76	2D	302	3PH	P-O11	3.32	1.70	1.60
76	1A	406	3PH	P-O11	3.31	1.70	1.60
76	1K	102	3PH	P-O11	3.30	1.70	1.60
76	h	201	3PH	P-O11	3.30	1.70	1.60
76	c	101	3PH	P-O11	3.29	1.70	1.60
76	1E	402	3PH	P-O11	3.28	1.70	1.60
90	P	401	NDP	O2B-C2B	-3.28	1.32	1.44
76	2I	201	3PH	P-O11	3.28	1.70	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
76	V	601	3PH	P-O11	3.27	1.70	1.60
76	3D	302	3PH	P-O11	3.25	1.70	1.60
76	w	201	3PH	P-O11	3.25	1.70	1.60
76	R	401	3PH	P-O11	3.25	1.70	1.60
76	S	301	3PH	P-O11	3.24	1.70	1.60
74	1B	403	HEM	CAB-C3B	3.23	1.56	1.47
76	1B	406	3PH	P-O11	3.22	1.70	1.60
76	1R	201	3PH	P-O11	3.20	1.70	1.60
76	g	101	3PH	P-O11	3.19	1.70	1.60
76	3I	201	3PH	P-O11	3.16	1.70	1.60
82	2A	602	HEA	FE-NB	3.10	2.12	1.96
82	2A	603	HEA	FE-ND	3.09	2.12	1.96
74	1B	404	HEM	CAB-C3B	3.07	1.55	1.47
74	1A	403	HEM	CAB-C3B	3.06	1.55	1.47
82	2A	603	HEA	C4B-C3B	3.06	1.49	1.44
82	2A	602	HEA	FE-ND	3.04	2.11	1.96
82	2A	603	HEA	C1D-ND	-3.03	1.35	1.40
82	3A	603	HEA	FE-ND	3.03	2.11	1.96
82	3A	602	HEA	FE-NB	3.01	2.11	1.96
82	3A	603	HEA	C1D-ND	-3.00	1.35	1.40
82	3A	603	HEA	C4B-C3B	2.98	1.49	1.44
82	2A	603	HEA	FE-NB	2.97	2.11	1.96
82	3A	603	HEA	FE-NB	2.97	2.11	1.96
74	1A	404	HEM	CAB-C3B	2.96	1.55	1.47
82	3A	602	HEA	FE-ND	2.95	2.11	1.96
82	3A	602	HEA	C1D-ND	-2.85	1.35	1.40
82	3A	602	HEA	C4B-C3B	2.83	1.49	1.44
82	2A	602	HEA	C2A-C1A	2.80	1.48	1.42
82	2A	602	HEA	C4B-NB	-2.77	1.35	1.40
82	3A	603	HEA	C4B-NB	-2.74	1.35	1.40
82	2A	602	HEA	C1D-ND	-2.70	1.35	1.40
82	3A	602	HEA	C4B-NB	-2.68	1.35	1.40
82	2A	603	HEA	C2A-C1A	2.64	1.48	1.42
89	r	200	8Q1	C1-S44	2.55	1.82	1.76
82	3A	602	HEA	C2A-C1A	2.51	1.48	1.42
91	s	401	COO	C5A-C4A	2.43	1.47	1.40
82	2A	603	HEA	C4B-NB	-2.43	1.36	1.40
89	r	200	8Q1	C6-C1	2.42	1.53	1.50
82	2A	603	HEA	C1C-CHC	2.42	1.47	1.41
89	r	200	8Q1	O40-C39	-2.39	1.18	1.23
82	3A	603	HEA	C2A-C1A	2.37	1.47	1.42
82	2A	602	HEA	C4B-C3B	2.36	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	J	200	8Q1	O40-C39	-2.36	1.18	1.23
82	2A	602	HEA	C4C-CHD	2.36	1.47	1.41
82	2A	603	HEA	C4D-C3D	2.35	1.49	1.45
82	3A	603	HEA	C1C-CHC	2.32	1.47	1.41
75	1M	501	CDL	PB2-OB4	-2.32	1.44	1.55
89	J	200	8Q1	C1-S44	2.31	1.81	1.76
90	P	401	NDP	C7N-C3N	-2.29	1.43	1.48
89	J	200	8Q1	C6-C1	2.25	1.53	1.50
82	3A	603	HEA	C4D-C3D	2.20	1.48	1.45
82	3A	603	HEA	C4C-CHD	2.19	1.47	1.41
75	x	101	CDL	PB2-OB4	-2.19	1.45	1.55
90	P	401	NDP	O3D-C3D	-2.18	1.37	1.43
82	2A	603	HEA	C4C-CHD	2.16	1.47	1.41
82	3A	602	HEA	C4C-CHD	2.15	1.47	1.41
82	2A	602	HEA	C1D-C2D	2.14	1.48	1.44
82	3A	602	HEA	C1C-CHC	2.13	1.46	1.41
87	B	501	FMN	C10-N1	2.13	1.37	1.33
90	P	401	NDP	O2D-C2D	-2.12	1.38	1.43
82	3A	602	HEA	C1D-C2D	2.12	1.48	1.44
82	2A	602	HEA	C1B-C2B	2.09	1.48	1.44
74	1B	403	HEM	CAA-C2A	2.08	1.55	1.52
74	1A	403	HEM	CAA-C2A	2.06	1.55	1.52
82	2A	602	HEA	C1C-CHC	2.06	1.46	1.41
82	3A	602	HEA	C4D-ND	-2.03	1.34	1.38
75	1B	405	CDL	PA1-OA4	-2.02	1.45	1.55
82	2A	602	HEA	CHB-C1B	2.02	1.46	1.41
82	2A	603	HEA	C1D-C2D	2.02	1.48	1.44
75	y	202	CDL	PB2-OB4	-2.01	1.45	1.55

All (231) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	s	401	COO	C15-C11-C12	-19.13	77.03	108.23
76	h	201	3PH	O31-C31-O32	-17.93	78.33	123.59
91	s	401	COO	C15-C11-C13	-16.74	79.80	108.82
91	s	401	COO	C15-C11-C14	-15.18	78.23	109.17
76	h	201	3PH	O31-C31-C32	14.35	156.94	111.91
76	h	201	3PH	O32-C31-C32	-11.56	78.63	123.73
82	3A	603	HEA	C3D-C4D-ND	6.87	117.00	110.36
82	2A	602	HEA	C3D-C4D-ND	6.79	116.93	110.36
82	2A	603	HEA	C3D-C4D-ND	6.75	116.90	110.36
89	J	200	8Q1	C6-C1-S44	6.65	121.19	113.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
90	P	401	NDP	PN-O3-PA	-6.31	111.17	132.83
82	3A	602	HEA	C3D-C4D-ND	6.19	116.35	110.36
82	3A	603	HEA	C2B-C1B-NB	5.74	116.75	109.88
82	3A	602	HEA	C2D-C1D-ND	5.71	116.61	109.84
82	2A	603	HEA	C2B-C1B-NB	5.66	116.66	109.88
82	2A	603	HEA	C2D-C1D-ND	5.61	116.49	109.84
82	2A	602	HEA	C3B-C4B-NB	5.59	116.46	109.84
82	3A	602	HEA	C2B-C1B-NB	5.51	116.48	109.88
89	r	200	8Q1	C6-C1-S44	5.50	119.86	113.46
82	3A	603	HEA	C2D-C1D-ND	5.38	116.21	109.84
82	2A	602	HEA	C2D-C1D-ND	5.27	116.08	109.84
73	1B	402	UQ5	C7-C6-C5	5.15	124.67	118.48
82	3A	602	HEA	C1D-C2D-C3D	-5.13	101.56	106.96
82	3A	602	HEA	C3B-C4B-NB	5.05	115.83	109.84
89	r	200	8Q1	C32-C34-N36	5.00	126.53	116.58
91	s	401	COO	C14-C11-C12	4.96	116.33	108.23
82	2A	602	HEA	C2B-C1B-NB	4.95	115.81	109.88
82	2A	603	HEA	C3B-C4B-NB	4.92	115.67	109.84
82	3A	603	HEA	C3B-C4B-NB	4.86	115.60	109.84
82	2A	602	HEA	C13-C12-C11	-4.45	107.67	114.35
73	1B	402	UQ5	C6-C1-C2	4.42	122.67	119.18
74	1A	403	HEM	C3B-C2B-C1B	4.35	109.71	106.49
82	2A	603	HEA	C3C-C4C-NC	4.20	114.64	109.21
82	3A	602	HEA	C3C-C4C-NC	4.17	114.60	109.21
78	1F	402	HEC	CMB-C2B-C1B	-4.15	122.09	128.46
82	2A	602	HEA	C1D-C2D-C3D	-4.10	102.64	106.96
82	3A	603	HEA	C3C-C4C-NC	4.10	114.51	109.21
91	s	401	COO	C14-C11-C13	4.05	115.84	108.82
74	1A	403	HEM	CMB-C2B-C1B	-4.03	118.90	125.04
82	3A	603	HEA	CBA-CAA-C2A	-4.02	105.83	112.60
82	3A	603	HEA	CMC-C2C-C3C	3.97	132.12	124.68
74	1A	404	HEM	CMC-C2C-C3C	3.95	132.06	124.68
78	1E	404	HEC	CMB-C2B-C1B	-3.89	122.48	128.46
82	2A	602	HEA	CMC-C2C-C3C	3.89	131.96	124.68
82	3A	602	HEA	CMC-C2C-C3C	3.88	131.94	124.68
89	J	200	8Q1	O4-C1-C6	-3.86	119.43	123.99
82	2A	602	HEA	C3C-C4C-NC	3.80	114.13	109.21
82	2A	603	HEA	C1D-C2D-C3D	-3.80	102.96	106.96
78	1E	404	HEC	CMC-C2C-C1C	-3.76	122.69	128.46
82	3A	603	HEA	CHA-C4D-ND	-3.71	120.40	124.43
82	3A	603	HEA	C1D-C2D-C3D	-3.67	103.10	106.96
82	3A	602	HEA	CBA-CAA-C2A	-3.65	106.44	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	3A	603	HEA	C4D-C3D-C2D	-3.65	101.57	106.90
82	2A	603	HEA	C4D-C3D-C2D	-3.65	101.58	106.90
82	3A	603	HEA	C27-C19-C20	3.64	121.40	115.27
74	1A	404	HEM	CMA-C3A-C4A	-3.64	122.88	128.46
73	1B	402	UQ5	C8-C7-C6	3.60	121.76	112.05
82	3A	603	HEA	C1B-C2B-C3B	-3.55	102.55	106.80
82	3A	602	HEA	CAD-CBD-CGD	-3.54	105.98	113.60
82	2A	603	HEA	CHA-C4D-ND	-3.54	120.58	124.43
78	1E	404	HEC	CMB-C2B-C3B	3.54	129.98	125.82
73	1A	401	UQ5	C8-C7-C6	3.53	121.55	112.05
73	1A	401	UQ5	C7-C6-C5	3.47	122.65	118.48
82	2A	603	HEA	CBA-CAA-C2A	-3.47	106.76	112.60
74	1B	404	HEM	CMC-C2C-C3C	3.47	131.16	124.68
82	3A	603	HEA	CAD-C3D-C4D	3.43	130.64	124.66
76	V	602	3PH	C2-O21-C21	3.35	126.03	117.79
82	3A	602	HEA	C1B-C2B-C3B	-3.33	102.82	106.80
82	2A	603	HEA	C1B-C2B-C3B	-3.33	102.82	106.80
82	2A	602	HEA	C4D-C3D-C2D	-3.32	102.06	106.90
89	r	200	8Q1	C37-C38-C39	-3.32	106.83	112.36
74	1B	403	HEM	C4C-CHD-C1D	3.32	126.93	122.56
90	P	401	NDP	O2B-P2B-O1X	-3.28	96.73	109.39
74	1A	403	HEM	C4C-CHD-C1D	3.28	126.88	122.56
82	2A	602	HEA	CMB-C2B-C1B	3.25	129.98	125.04
89	r	200	8Q1	O4-C1-C6	-3.24	120.16	123.99
82	3A	602	HEA	C13-C12-C11	-3.22	109.52	114.35
74	1B	403	HEM	C3B-C2B-C1B	3.21	108.87	106.49
78	1F	402	HEC	CMC-C2C-C1C	-3.18	123.58	128.46
91	s	401	COO	N3A-C2A-N1A	-3.17	123.72	128.68
74	1A	403	HEM	CHB-C1B-NB	3.16	128.28	124.38
74	1A	403	HEM	CMC-C2C-C3C	3.15	130.58	124.68
91	s	401	COO	P1A-O3A-P2A	-3.14	122.05	132.83
87	B	501	FMN	C4-N3-C2	-3.12	119.88	125.64
82	2A	603	HEA	C4B-C3B-C2B	-3.11	102.10	107.41
90	P	401	NDP	PA-O5B-C5B	-3.10	103.49	121.68
82	2A	602	HEA	C4B-C3B-C2B	-3.09	102.12	107.41
82	2A	602	HEA	C1B-C2B-C3B	-3.08	103.12	106.80
89	r	200	8Q1	O35-C34-N36	-3.06	116.42	122.99
77	T	501	PTY	C6-O7-C8	3.06	125.32	117.79
82	3A	602	HEA	C4B-C3B-C2B	-3.05	102.20	107.41
82	2A	603	HEA	C27-C19-C20	2.98	120.29	115.27
82	2A	603	HEA	CAD-C3D-C4D	2.98	129.87	124.66
82	2A	602	HEA	CAD-CBD-CGD	-2.98	107.19	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	1F	402	HEC	C1D-C2D-C3D	-2.97	104.93	107.00
74	1A	404	HEM	C4D-ND-C1D	2.97	108.14	105.07
91	s	401	COO	C4A-C5A-N7A	-2.94	106.33	109.40
82	3A	603	HEA	C4B-C3B-C2B	-2.94	102.39	107.41
91	s	401	COO	C3X-C2X-C1X	2.93	106.37	99.89
74	1A	403	HEM	C4D-ND-C1D	2.93	108.09	105.07
73	1A	401	UQ5	C6-C1-C2	2.92	121.49	119.18
82	2A	603	HEA	C1D-ND-C4D	-2.91	102.07	105.07
74	1B	403	HEM	C4D-ND-C1D	2.89	108.06	105.07
82	2A	603	HEA	CMC-C2C-C3C	2.89	130.09	124.68
73	1B	402	UQ5	O5-C5-C4	-2.89	114.80	120.93
91	s	401	COO	C10-C9-C8	-2.88	119.65	125.34
82	3A	603	HEA	C1D-ND-C4D	-2.87	102.11	105.07
82	2A	602	HEA	C13-C14-C15	-2.81	120.89	127.66
82	2A	603	HEA	CAD-CBD-CGD	-2.81	107.56	113.60
73	1A	402	UQ5	C7-C6-C5	-2.78	115.13	118.48
87	B	501	FMN	C4A-C10-N10	2.75	120.51	116.48
90	P	401	NDP	PN-O5D-C5D	-2.74	105.64	121.68
82	3A	602	HEA	CMD-C2D-C1D	2.73	129.20	125.04
82	3A	603	HEA	CHB-C1B-C2B	-2.73	120.71	124.98
74	1B	403	HEM	C4B-CHC-C1C	2.73	126.16	122.56
74	1B	404	HEM	C4D-ND-C1D	2.71	107.87	105.07
78	1F	402	HEC	CMB-C2B-C3B	2.71	129.01	125.82
78	1F	402	HEC	CAA-CBA-CGA	-2.71	106.17	113.76
87	B	501	FMN	C4A-C4-N3	2.71	120.06	113.19
82	2A	602	HEA	C1D-ND-C4D	-2.70	102.29	105.07
82	3A	602	HEA	C27-C19-C20	2.68	119.78	115.27
82	2A	603	HEA	C13-C14-C15	-2.67	121.23	127.66
82	3A	603	HEA	C13-C14-C15	-2.66	121.25	127.66
82	3A	602	HEA	CHA-C4D-C3D	-2.66	120.93	124.84
82	3A	603	HEA	CAD-CBD-CGD	-2.65	107.89	113.60
89	r	200	8Q1	C38-C39-N41	2.64	120.87	116.42
82	3A	602	HEA	C1D-ND-C4D	-2.64	102.34	105.07
89	r	200	8Q1	C43-S44-C1	2.64	110.08	101.87
82	2A	603	HEA	C26-C15-C16	2.63	119.69	115.27
82	2A	602	HEA	C27-C19-C20	2.62	119.68	115.27
78	1E	404	HEC	C1D-C2D-C3D	-2.61	105.18	107.00
82	3A	602	HEA	C4D-C3D-C2D	-2.59	103.13	106.90
82	3A	603	HEA	CMD-C2D-C1D	2.54	128.90	125.04
82	2A	602	HEA	C4B-NB-C1B	-2.52	102.47	105.07
90	P	401	NDP	O3X-P2B-O2X	2.50	117.17	107.64
74	1A	403	HEM	CHD-C1D-ND	2.49	127.14	124.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	J	200	8Q1	O4-C1-S44	-2.49	119.38	122.61
82	2A	603	HEA	CHB-C1B-C2B	-2.49	121.09	124.98
87	B	501	FMN	O4-C4-C4A	-2.46	120.07	126.60
82	3A	602	HEA	C13-C14-C15	-2.45	121.77	127.66
82	3A	602	HEA	C26-C15-C16	2.44	119.38	115.27
89	J	200	8Q1	C38-C39-N41	2.44	120.53	116.42
73	1A	401	UQ5	C7-C8-C9	-2.44	122.73	126.79
74	1A	403	HEM	CMA-C3A-C4A	-2.44	124.72	128.46
82	2A	602	HEA	CHA-C4D-C3D	-2.43	121.26	124.84
90	P	401	NDP	C5B-C4B-C3B	-2.42	106.12	115.18
82	2A	602	HEA	CHA-C4D-ND	-2.42	121.81	124.43
76	w	201	3PH	C2-O21-C21	2.42	123.74	117.79
73	Q	301	UQ5	C12-C13-C14	2.41	133.47	127.66
82	2A	602	HEA	CBA-CAA-C2A	-2.41	108.54	112.60
76	w	201	3PH	O13-P-O11	-2.40	100.35	106.73
90	P	401	NDP	O4B-C4B-C3B	2.38	109.83	105.11
82	3A	602	HEA	CMB-C2B-C1B	2.38	128.66	125.04
74	1B	404	HEM	C1B-NB-C4B	2.37	107.53	105.07
73	1B	402	UQ5	C1-C6-C5	-2.37	117.35	119.58
74	1A	403	HEM	C1B-NB-C4B	2.37	107.52	105.07
74	1B	403	HEM	CMA-C3A-C4A	-2.36	124.83	128.46
79	u	601	PC7	O3-C3-C2	2.36	115.29	108.43
73	Q	301	UQ5	C8-C7-C6	2.35	118.39	112.05
82	2A	602	HEA	CHB-C1B-NB	-2.34	121.89	124.43
82	2A	603	HEA	C25-C23-C24	2.34	119.77	114.60
89	J	200	8Q1	C43-S44-C1	2.34	109.15	101.87
82	3A	602	HEA	CHB-C1B-C2B	-2.33	121.34	124.98
74	1B	404	HEM	C3D-C4D-ND	-2.33	107.57	110.17
76	3I	201	3PH	O13-P-O11	-2.33	100.54	106.73
74	1A	404	HEM	C4C-CHD-C1D	2.32	125.63	122.56
74	1B	404	HEM	C4B-CHC-C1C	2.32	125.62	122.56
82	3A	602	HEA	C4B-NB-C1B	-2.32	102.67	105.07
76	3D	302	3PH	O13-P-O11	-2.32	100.56	106.73
74	1A	404	HEM	C3D-C4D-ND	-2.30	107.61	110.17
82	3A	603	HEA	C4B-NB-C1B	-2.30	102.70	105.07
78	1F	402	HEC	CBD-CAD-C3D	-2.29	108.71	112.62
73	Q	301	UQ5	C12-C11-C9	2.29	120.50	112.98
90	P	401	NDP	C3N-C2N-N1N	-2.28	119.85	123.10
76	1R	201	3PH	O13-P-O11	-2.27	100.68	106.73
89	r	200	8Q1	C37-N36-C34	2.27	126.64	122.59
87	B	501	FMN	C4A-C10-N1	-2.27	119.47	124.73
74	1A	404	HEM	CMB-C2B-C1B	-2.26	121.59	125.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	2A	603	HEA	C4B-NB-C1B	-2.25	102.75	105.07
81	T	502	PGT	C3-C2-C1	2.25	117.11	111.79
82	2A	603	HEA	CHD-C1D-C2D	-2.25	120.50	126.72
76	1B	406	3PH	O13-P-O11	-2.23	100.80	106.73
82	3A	603	HEA	C25-C23-C24	2.23	119.53	114.60
87	B	501	FMN	C10-C4A-N5	-2.22	120.14	124.86
74	1A	404	HEM	C4A-C3A-C2A	2.22	108.54	107.00
90	P	401	NDP	O7N-C7N-C3N	2.21	125.07	120.90
76	y	201	3PH	O13-P-O11	-2.21	100.84	106.73
74	1B	403	HEM	CBD-CAD-C3D	-2.20	106.52	112.63
76	1A	406	3PH	O13-P-O11	-2.19	100.92	106.73
78	1E	404	HEC	CAA-CBA-CGA	-2.18	107.64	113.76
76	2I	201	3PH	O13-P-O11	-2.17	100.95	106.73
81	l	701	PGT	C2-O2-C31	2.17	123.14	117.79
82	2A	602	HEA	CHD-C1D-C2D	-2.16	120.74	126.72
74	1B	404	HEM	CBD-CAD-C3D	-2.16	106.63	112.63
89	r	200	8Q1	C31-C29-C32	2.15	112.55	108.82
74	1A	403	HEM	C4B-CHC-C1C	2.15	125.40	122.56
90	P	401	NDP	C2A-N1A-C6A	-2.14	115.09	118.75
76	c	101	3PH	O13-P-O11	-2.14	101.03	106.73
82	3A	602	HEA	CHD-C1D-C2D	-2.14	120.80	126.72
73	1B	402	UQ5	O5-C5-C6	2.13	125.29	121.55
76	h	201	3PH	O14-P-O13	2.13	115.77	107.64
73	1B	401	UQ5	C7-C6-C5	-2.13	115.92	118.48
82	3A	603	HEA	C26-C15-C16	2.12	118.84	115.27
74	1B	403	HEM	C3D-C4D-ND	-2.12	107.81	110.17
76	1K	102	3PH	O13-P-O11	-2.11	101.12	106.73
82	2A	602	HEA	C26-C15-C16	2.10	118.81	115.27
76	g	101	3PH	O13-P-O11	-2.10	101.14	106.73
76	R	401	3PH	O13-P-O11	-2.09	101.17	106.73
76	S	301	3PH	O13-P-O11	-2.09	101.17	106.73
82	3A	602	HEA	C25-C23-C24	2.09	119.22	114.60
82	3A	602	HEA	CHB-C1B-NB	-2.07	122.18	124.43
90	P	401	NDP	C3B-C2B-C1B	-2.07	99.00	102.89
90	P	401	NDP	O5D-PN-O1N	-2.07	100.98	109.07
74	1B	404	HEM	C4C-CHD-C1D	2.06	125.28	122.56
87	B	501	FMN	C9A-C5A-N5	-2.06	120.19	122.43
76	h	201	3PH	O13-P-O11	-2.06	101.24	106.73
82	3A	603	HEA	CHD-C1D-C2D	-2.06	121.02	126.72
76	2D	302	3PH	O13-P-O11	-2.05	101.28	106.73
82	2A	602	HEA	C25-C23-C24	2.04	119.12	114.60
79	1G	301	PC7	C3-C2-C1	2.04	116.62	111.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	V	601	3PH	O13-P-O11	-2.04	101.31	106.73
79	u	601	PC7	C3-C2-C1	2.03	116.59	111.79
89	r	200	8Q1	O4-C1-S44	-2.03	119.98	122.61
90	P	401	NDP	O2N-PN-O1N	2.03	122.27	112.24
87	B	501	FMN	C5A-C9A-N10	2.02	120.04	117.95
76	1K	102	3PH	O14-P-O13	2.02	115.37	107.64
76	R	401	3PH	O14-P-O13	2.02	115.35	107.64
76	w	201	3PH	O14-P-O13	2.02	115.35	107.64
74	1A	403	HEM	C2D-C1D-ND	-2.02	107.47	109.88
82	2A	602	HEA	C17-C18-C19	-2.00	122.83	127.66
82	2A	603	HEA	CHB-C1B-NB	-2.00	122.25	124.43

There are no chirality outliers.

All (1751) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
73	1A	401	UQ5	C1-C6-C7-C8
73	1A	401	UQ5	C5-C6-C7-C8
73	1A	401	UQ5	C9-C11-C12-C13
73	1A	401	UQ5	C24-C26-C27-C28
73	1A	402	UQ5	C14-C16-C17-C18
73	1B	401	UQ5	C9-C11-C12-C13
73	1B	401	UQ5	C20-C19-C21-C22
73	1B	401	UQ5	C19-C21-C22-C23
73	1B	402	UQ5	C1-C6-C7-C8
73	1B	402	UQ5	C5-C6-C7-C8
73	1B	402	UQ5	C13-C14-C16-C17
73	1B	402	UQ5	C15-C14-C16-C17
73	1B	402	UQ5	C14-C16-C17-C18
73	1B	402	UQ5	C19-C21-C22-C23
73	1B	402	UQ5	C24-C26-C27-C28
73	Q	301	UQ5	C19-C21-C22-C23
74	1B	404	HEM	C2A-CAA-CBA-CGA
75	1A	405	CDL	O1-C1-CB2-OB2
75	1A	405	CDL	CA3-OA5-PA1-OA3
75	1A	405	CDL	CA3-OA5-PA1-OA4
75	1A	405	CDL	CB2-OB2-PB2-OB3
75	1A	405	CDL	CB2-OB2-PB2-OB4
75	1A	405	CDL	CB2-OB2-PB2-OB5
75	1A	405	CDL	CB3-OB5-PB2-OB4
75	1A	405	CDL	C51-CB5-OB6-CB4
75	1B	405	CDL	CA3-OA5-PA1-OA4

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Mol	Chain	Res	Type	Atoms
75	1B	405	CDL	C11-CA5-OA6-CA4
75	1B	405	CDL	CB3-OB5-PB2-OB3
75	1B	405	CDL	OB7-CB5-OB6-CB4
75	1B	405	CDL	C51-CB5-OB6-CB4
75	1B	408	CDL	CA2-OA2-PA1-OA3
75	1B	408	CDL	CA2-OA2-PA1-OA4
75	1B	408	CDL	CA2-OA2-PA1-OA5
75	1B	408	CDL	OA6-CA4-CA6-OA8
75	1B	408	CDL	OA7-CA5-OA6-CA4
75	1E	401	CDL	O1-C1-CB2-OB2
75	1E	401	CDL	CA2-OA2-PA1-OA3
75	1E	401	CDL	CA2-OA2-PA1-OA4
75	1E	401	CDL	CA3-OA5-PA1-OA3
75	1E	401	CDL	C11-CA5-OA6-CA4
75	1E	401	CDL	CB2-OB2-PB2-OB3
75	1E	401	CDL	CB2-OB2-PB2-OB4
75	1E	401	CDL	OB7-CB5-OB6-CB4
75	1E	401	CDL	C51-CB5-OB6-CB4
75	1F	401	CDL	CA3-OA5-PA1-OA2
75	1F	401	CDL	CA3-OA5-PA1-OA3
75	1F	401	CDL	CA3-OA5-PA1-OA4
75	1F	401	CDL	CB2-OB2-PB2-OB3
75	1F	401	CDL	CB2-OB2-PB2-OB4
75	1F	401	CDL	CB2-OB2-PB2-OB5
75	1F	401	CDL	OB5-CB3-CB4-OB6
75	1F	401	CDL	C51-CB5-OB6-CB4
75	1K	101	CDL	CA3-OA5-PA1-OA2
75	1K	101	CDL	CB2-OB2-PB2-OB3
75	1K	101	CDL	CB2-OB2-PB2-OB4
75	1K	101	CDL	CB3-OB5-PB2-OB3
75	1L	101	CDL	CA2-OA2-PA1-OA4
75	1L	101	CDL	CA3-OA5-PA1-OA3
75	1L	101	CDL	OA7-CA5-OA6-CA4
75	1L	101	CDL	CB2-OB2-PB2-OB3
75	1L	101	CDL	CB2-OB2-PB2-OB4
75	1L	101	CDL	CB3-OB5-PB2-OB2
75	1L	101	CDL	CB3-OB5-PB2-OB3
75	1L	101	CDL	CB3-OB5-PB2-OB4
75	1M	501	CDL	CA2-OA2-PA1-OA3
75	1M	501	CDL	CA2-OA2-PA1-OA4
75	1M	501	CDL	CA2-OA2-PA1-OA5
75	1M	501	CDL	OB6-CB4-CB6-OB8

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Mol	Chain	Res	Type	Atoms
75	1M	501	CDL	C51-CB5-OB6-CB4
75	R	405	CDL	CA2-OA2-PA1-OA3
75	R	405	CDL	CA2-OA2-PA1-OA4
75	R	405	CDL	CA3-OA5-PA1-OA2
75	R	405	CDL	CA3-OA5-PA1-OA3
75	R	405	CDL	CA3-OA5-PA1-OA4
75	R	405	CDL	CB2-OB2-PB2-OB3
75	R	405	CDL	CB2-OB2-PB2-OB4
75	R	405	CDL	CB2-OB2-PB2-OB5
75	R	405	CDL	CB3-OB5-PB2-OB3
75	R	405	CDL	OB5-CB3-CB4-OB6
75	R	405	CDL	C51-CB5-OB6-CB4
75	V	603	CDL	CA2-OA2-PA1-OA3
75	V	603	CDL	C11-CA5-OA6-CA4
75	V	603	CDL	CB2-OB2-PB2-OB4
75	V	603	CDL	CB3-OB5-PB2-OB3
75	V	603	CDL	CB3-OB5-PB2-OB4
75	W	701	CDL	CA2-OA2-PA1-OA3
75	W	701	CDL	CA3-OA5-PA1-OA2
75	W	701	CDL	CA3-OA5-PA1-OA3
75	W	701	CDL	CA3-OA5-PA1-OA4
75	W	701	CDL	OA7-CA5-OA6-CA4
75	W	701	CDL	C11-CA5-OA6-CA4
75	h	203	CDL	CA2-C1-CB2-OB2
75	h	203	CDL	CA2-OA2-PA1-OA3
75	h	203	CDL	CA2-OA2-PA1-OA4
75	h	203	CDL	CA2-OA2-PA1-OA5
75	h	203	CDL	CA3-OA5-PA1-OA3
75	h	203	CDL	CA3-OA5-PA1-OA4
75	h	203	CDL	CB2-OB2-PB2-OB3
75	h	203	CDL	CB2-OB2-PB2-OB5
75	h	203	CDL	CB3-OB5-PB2-OB3
75	u	602	CDL	CA2-C1-CB2-OB2
75	u	602	CDL	CA2-OA2-PA1-OA3
75	u	602	CDL	CA2-OA2-PA1-OA4
75	u	602	CDL	CA2-OA2-PA1-OA5
75	u	602	CDL	CA3-OA5-PA1-OA2
75	u	602	CDL	CA3-OA5-PA1-OA3
75	u	602	CDL	CA3-OA5-PA1-OA4
75	u	602	CDL	C51-CB5-OB6-CB4
75	u	603	CDL	O1-C1-CB2-OB2
75	u	603	CDL	CA2-OA2-PA1-OA4

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Mol	Chain	Res	Type	Atoms
75	u	603	CDL	CA3-OA5-PA1-OA3
75	u	603	CDL	CB2-OB2-PB2-OB4
75	u	603	CDL	CB3-OB5-PB2-OB3
75	x	101	CDL	CA3-OA5-PA1-OA4
75	x	101	CDL	CB2-OB2-PB2-OB3
75	y	202	CDL	O1-C1-CB2-OB2
75	y	202	CDL	CA2-C1-CB2-OB2
75	y	202	CDL	CA3-OA5-PA1-OA3
75	y	202	CDL	CA3-OA5-PA1-OA4
76	1A	406	3PH	C22-C21-O21-C2
76	1B	406	3PH	C1-O11-P-O13
76	1B	406	3PH	C1-O11-P-O14
76	1B	406	3PH	C1-O11-P-O12
76	1B	407	3PH	C1-O11-P-O13
76	1B	407	3PH	C1-O11-P-O14
76	1B	407	3PH	C1-O11-P-O12
76	1E	402	3PH	C1-O11-P-O13
76	1E	402	3PH	C1-O11-P-O14
76	1E	402	3PH	C1-O11-P-O12
76	1E	402	3PH	O21-C2-C3-O31
76	2D	302	3PH	C1-O11-P-O13
76	2D	302	3PH	C1-O11-P-O14
76	2D	302	3PH	C1-O11-P-O12
76	2D	302	3PH	C22-C21-O21-C2
76	2I	201	3PH	C1-O11-P-O13
76	2I	201	3PH	C1-O11-P-O14
76	3D	302	3PH	C1-O11-P-O13
76	3D	302	3PH	C1-O11-P-O14
76	3D	302	3PH	C1-O11-P-O12
76	3D	302	3PH	O22-C21-O21-C2
76	3D	302	3PH	C22-C21-O21-C2
76	R	401	3PH	C1-O11-P-O13
76	R	401	3PH	C1-O11-P-O14
76	S	301	3PH	C1-O11-P-O13
76	S	301	3PH	C1-O11-P-O14
76	S	301	3PH	C1-O11-P-O12
76	V	601	3PH	C1-O11-P-O13
76	V	601	3PH	C1-O11-P-O14
76	V	601	3PH	O22-C21-O21-C2
76	V	601	3PH	C22-C21-O21-C2
76	V	602	3PH	C1-O11-P-O13
76	V	602	3PH	C1-O11-P-O14

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Mol	Chain	Res	Type	Atoms
76	V	602	3PH	C1-O11-P-O12
76	V	602	3PH	C22-C21-O21-C2
76	c	101	3PH	C1-O11-P-O13
76	c	101	3PH	C1-O11-P-O14
76	c	101	3PH	C1-O11-P-O12
76	h	201	3PH	C1-O11-P-O13
76	h	201	3PH	C1-O11-P-O14
76	h	201	3PH	O11-C1-C2-O21
76	h	201	3PH	C22-C21-O21-C2
76	y	201	3PH	C1-O11-P-O13
76	y	201	3PH	C1-O11-P-O14
76	y	201	3PH	C1-O11-P-O12
77	1F	403	PTY	C3-O11-P1-O12
77	2D	301	PTY	C11-C8-O7-C6
77	2F	101	PTY	C3-O11-P1-O12
77	2F	101	PTY	C5-O14-P1-O11
77	2F	101	PTY	C5-O14-P1-O13
77	3D	301	PTY	N1-C2-C3-O11
77	3D	301	PTY	C11-C8-O7-C6
77	3F	101	PTY	N1-C2-C3-O11
77	3F	101	PTY	C11-C8-O7-C6
77	3F	101	PTY	C3-O11-P1-O14
77	3F	101	PTY	C5-O14-P1-O11
77	G	303	PTY	C3-O11-P1-O13
77	R	402	PTY	C2-C3-O11-P1
77	R	402	PTY	C6-C5-O14-P1
77	R	402	PTY	C3-O11-P1-O12
77	R	404	PTY	C11-C8-O7-C6
77	R	404	PTY	C5-O14-P1-O12
77	R	406	PTY	O14-C5-C6-O7
77	R	406	PTY	C11-C8-O7-C6
77	R	406	PTY	C5-O14-P1-O11
77	S	302	PTY	C3-O11-P1-O12
77	S	302	PTY	C5-O14-P1-O13
77	T	501	PTY	N1-C2-C3-O11
77	T	501	PTY	C3-O11-P1-O12
77	T	501	PTY	C5-O14-P1-O11
77	T	504	PTY	N1-C2-C3-O11
77	T	504	PTY	C5-O14-P1-O12
77	V	604	PTY	N1-C2-C3-O11
77	V	604	PTY	C3-O11-P1-O12
77	V	604	PTY	C3-O11-P1-O13

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Mol	Chain	Res	Type	Atoms
77	V	605	PTY	N1-C2-C3-O11
77	V	605	PTY	C3-O11-P1-O13
77	V	605	PTY	C5-O14-P1-O12
77	e	301	PTY	N1-C2-C3-O11
77	e	301	PTY	C3-O11-P1-O13
77	e	301	PTY	C3-O11-P1-O14
77	e	302	PTY	O14-C5-C6-O7
77	e	302	PTY	O10-C8-O7-C6
77	e	302	PTY	C11-C8-O7-C6
77	e	302	PTY	C5-O14-P1-O12
77	h	202	PTY	O10-C8-O7-C6
77	h	202	PTY	C3-O11-P1-O14
77	h	202	PTY	C5-O14-P1-O12
77	x	102	PTY	O10-C8-O7-C6
77	x	102	PTY	C3-O11-P1-O13
79	1G	301	PC7	C4-O4P-P-O2P
79	1H	101	PC7	C1-O3P-P-O2P
79	1H	101	PC7	C4-O4P-P-O2P
79	1H	101	PC7	O4P-C4-C5-N
79	3A	606	PC7	C2-C1-O3P-P
79	3A	606	PC7	C1-O3P-P-O1P
79	3A	606	PC7	C1-O3P-P-O2P
79	3A	606	PC7	C1-O3P-P-O4P
79	3A	606	PC7	C4-O4P-P-O2P
79	Q	302	PC7	C4-O4P-P-O3P
79	Q	302	PC7	C4-O4P-P-O1P
79	Q	302	PC7	C4-O4P-P-O2P
79	R	403	PC7	C1-O3P-P-O1P
79	R	403	PC7	C1-O3P-P-O2P
79	R	403	PC7	C1-O3P-P-O4P
79	R	403	PC7	O4P-C4-C5-N
79	T	503	PC7	C32-C31-O2-C2
79	T	503	PC7	C4-O4P-P-O2P
79	T	503	PC7	O4P-C4-C5-N
79	u	601	PC7	C32-C31-O2-C2
79	u	601	PC7	C4-O4P-P-O1P
81	3A	601	PGT	C1-O3P-P-O1P
81	T	502	PGT	C4-O4P-P-O1P
81	T	505	PGT	C1-O3P-P-O4P
81	b	601	PGT	C2-C1-O3P-P
81	b	601	PGT	C1-O3P-P-O2P
81	b	601	PGT	C4-O4P-P-O1P

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Mol	Chain	Res	Type	Atoms
81	l	701	PGT	O3P-C1-C2-O2
81	l	701	PGT	C4-O4P-P-O1P
82	2A	603	HEA	C3B-C11-C12-C13
82	2A	603	HEA	O11-C11-C12-C13
82	2A	603	HEA	C15-C16-C17-C18
82	3A	603	HEA	C3B-C11-C12-C13
82	3A	603	HEA	O11-C11-C12-C13
82	3A	603	HEA	C15-C16-C17-C18
82	3A	603	HEA	C19-C20-C21-C22
87	B	501	FMN	C5'-O5'-P-O1P
87	B	501	FMN	C5'-O5'-P-O2P
87	B	501	FMN	C5'-O5'-P-O3P
89	J	200	8Q1	C1-C6-C7-C8
89	J	200	8Q1	O27-C28-C29-C32
89	r	200	8Q1	C1-C6-C7-C8
89	r	200	8Q1	O4-C1-S44-C43
89	r	200	8Q1	C6-C1-S44-C43
89	r	200	8Q1	C28-C29-C32-C34
89	r	200	8Q1	C28-C29-C32-O33
89	r	200	8Q1	C30-C29-C32-C34
89	r	200	8Q1	C30-C29-C32-O33
89	r	200	8Q1	C31-C29-C32-C34
89	r	200	8Q1	C31-C29-C32-O33
89	r	200	8Q1	O33-C32-C34-N36
89	r	200	8Q1	C32-C34-N36-C37
89	r	200	8Q1	C28-O27-P24-O1
90	P	401	NDP	C5B-O5B-PA-O2A
90	P	401	NDP	C5B-O5B-PA-O3
90	P	401	NDP	O4B-C4B-C5B-O5B
90	P	401	NDP	C3B-C4B-C5B-O5B
90	P	401	NDP	C5D-O5D-PN-O3
90	P	401	NDP	C5D-O5D-PN-O1N
91	s	401	COO	C14-C11-C13-O1
91	s	401	COO	C12-C11-C13-O1
91	s	401	COO	C14-C11-C13-C1
91	s	401	COO	C12-C11-C13-C1
91	s	401	COO	C13-C11-C12-O6A
91	s	401	COO	C13-C1-N1-C2
91	s	401	COO	O2-C1-N1-C2
91	s	401	COO	C3-C4-N2-C5
91	s	401	COO	O3-C4-N2-C5
91	s	401	COO	O4-C7-S1-C6

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Mol	Chain	Res	Type	Atoms
91	s	401	COO	C8-C7-S1-C6
91	s	401	COO	S1-C7-C8-C9
75	1M	501	CDL	OA9-CA7-OA8-CA6
75	V	603	CDL	OB9-CB7-OB8-CB6
75	W	701	CDL	OB9-CB7-OB8-CB6
75	u	602	CDL	OA9-CA7-OA8-CA6
76	g	101	3PH	O32-C31-O31-C3
77	R	404	PTY	O30-C30-O4-C1
77	V	606	PTY	O30-C30-O4-C1
81	l	701	PGT	O11-C11-O3-C3
75	V	603	CDL	C71-CB7-OB8-CB6
75	u	602	CDL	C31-CA7-OA8-CA6
77	R	404	PTY	C31-C30-O4-C1
77	V	606	PTY	C31-C30-O4-C1
81	b	601	PGT	C12-C11-O3-C3
75	1F	401	CDL	OB9-CB7-OB8-CB6
75	1K	101	CDL	OB9-CB7-OB8-CB6
76	1B	406	3PH	O32-C31-O31-C3
76	1B	407	3PH	O32-C31-O31-C3
76	h	201	3PH	O32-C31-O31-C3
77	h	202	PTY	O30-C30-O4-C1
79	2A	606	PC7	O11-C11-O3-C3
81	b	601	PGT	O11-C11-O3-C3
75	1A	405	CDL	OB7-CB5-OB6-CB4
75	1B	405	CDL	OA7-CA5-OA6-CA4
75	1E	401	CDL	OA7-CA5-OA6-CA4
75	1F	401	CDL	OB7-CB5-OB6-CB4
75	1K	101	CDL	OB7-CB5-OB6-CB4
75	1M	501	CDL	OB7-CB5-OB6-CB4
75	R	405	CDL	OB7-CB5-OB6-CB4
75	V	603	CDL	OA7-CA5-OA6-CA4
75	W	701	CDL	OB7-CB5-OB6-CB4
75	u	602	CDL	OB7-CB5-OB6-CB4
76	1A	406	3PH	O22-C21-O21-C2
76	V	602	3PH	O22-C21-O21-C2
77	2D	301	PTY	O10-C8-O7-C6
77	3D	301	PTY	O10-C8-O7-C6
77	3F	101	PTY	O10-C8-O7-C6
77	R	404	PTY	O10-C8-O7-C6
77	R	406	PTY	O10-C8-O7-C6
79	T	503	PC7	O31-C31-O2-C2
79	u	601	PC7	O31-C31-O2-C2

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Mol	Chain	Res	Type	Atoms
77	1E	403	PTY	O30-C30-O4-C1
75	1E	401	CDL	C71-CB7-OB8-CB6
75	1F	401	CDL	C71-CB7-OB8-CB6
75	1M	501	CDL	C31-CA7-OA8-CA6
75	W	701	CDL	C71-CB7-OB8-CB6
76	1B	407	3PH	C32-C31-O31-C3
76	g	101	3PH	C32-C31-O31-C3
79	2A	606	PC7	C12-C11-O3-C3
81	T	505	PGT	C12-C11-O3-C3
81	l	701	PGT	C12-C11-O3-C3
75	1B	408	CDL	C11-CA5-OA6-CA4
75	1K	101	CDL	C51-CB5-OB6-CB4
75	1L	101	CDL	C11-CA5-OA6-CA4
77	h	202	PTY	C11-C8-O7-C6
77	x	102	PTY	C11-C8-O7-C6
79	3A	606	PC7	O11-C11-O3-C3
73	1B	401	UQ5	C15-C14-C16-C17
73	1B	401	UQ5	C18-C19-C21-C22
75	1B	405	CDL	C31-CA7-OA8-CA6
75	1K	101	CDL	C71-CB7-OB8-CB6
76	1B	406	3PH	C32-C31-O31-C3
76	1R	201	3PH	C32-C31-O31-C3
76	h	201	3PH	C32-C31-O31-C3
77	1E	403	PTY	C31-C30-O4-C1
77	h	202	PTY	C31-C30-O4-C1
81	2A	601	PGT	C12-C11-O3-C3
76	2D	302	3PH	O22-C21-O21-C2
76	h	201	3PH	O22-C21-O21-C2
75	1E	401	CDL	OB9-CB7-OB8-CB6
77	e	302	PTY	O30-C30-O4-C1
79	R	403	PC7	O11-C11-O3-C3
81	T	505	PGT	O11-C11-O3-C3
75	1B	405	CDL	O1-C1-CA2-OA2
75	1F	401	CDL	O1-C1-CB2-OB2
75	1K	101	CDL	O1-C1-CA2-OA2
75	1L	101	CDL	O1-C1-CB2-OB2
75	R	405	CDL	O1-C1-CA2-OA2
75	h	203	CDL	O1-C1-CB2-OB2
75	u	602	CDL	O1-C1-CB2-OB2
75	x	101	CDL	O1-C1-CB2-OB2
75	y	202	CDL	O1-C1-CA2-OA2
81	b	601	PGT	O4P-C4-C5-O5

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Mol	Chain	Res	Type	Atoms
75	u	603	CDL	C31-CA7-OA8-CA6
77	e	301	PTY	C31-C30-O4-C1
77	e	302	PTY	C31-C30-O4-C1
81	T	502	PGT	C12-C11-O3-C3
75	h	203	CDL	C71-C72-C73-C74
76	1R	201	3PH	O32-C31-O31-C3
89	r	200	8Q1	O35-C34-N36-C37
75	1L	101	CDL	C51-CB5-OB6-CB4
75	W	701	CDL	C51-CB5-OB6-CB4
77	T	501	PTY	C11-C8-O7-C6
75	h	203	CDL	C75-C76-C77-C78
81	T	502	PGT	O11-C11-O3-C3
75	x	101	CDL	C72-C73-C74-C75
75	u	603	CDL	C13-C14-C15-C16
90	P	401	NDP	O4D-C4D-C5D-O5D
79	3A	606	PC7	C12-C11-O3-C3
79	R	403	PC7	C12-C11-O3-C3
77	T	501	PTY	O10-C8-O7-C6
75	1B	405	CDL	OA9-CA7-OA8-CA6
75	u	603	CDL	OA9-CA7-OA8-CA6
81	2A	601	PGT	O11-C11-O3-C3
77	e	301	PTY	O30-C30-O4-C1
76	h	201	3PH	C3B-C3C-C3D-C3E
81	T	502	PGT	C17-C18-C19-C20
75	R	405	CDL	C71-CB7-OB8-CB6
79	1H	101	PC7	C12-C11-O3-C3
75	W	701	CDL	C63-C64-C65-C66
75	1A	405	CDL	C11-CA5-OA6-CA4
76	2I	201	3PH	C22-C21-O21-C2
76	S	301	3PH	C22-C21-O21-C2
75	1F	401	CDL	CA2-C1-CB2-OB2
75	1L	101	CDL	CA2-C1-CB2-OB2
75	W	701	CDL	CA2-C1-CB2-OB2
75	u	603	CDL	CA2-C1-CB2-OB2
75	y	202	CDL	CB2-C1-CA2-OA2
75	1L	101	CDL	OB7-CB5-OB6-CB4
75	R	405	CDL	OB9-CB7-OB8-CB6
79	Q	302	PC7	C4-C5-N-C7
75	1L	101	CDL	C31-CA7-OA8-CA6
75	x	101	CDL	C31-CA7-OA8-CA6
76	1E	402	3PH	C32-C31-O31-C3
76	1K	102	3PH	C32-C31-O31-C3

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Mol	Chain	Res	Type	Atoms
76	R	401	3PH	C32-C31-O31-C3
75	h	203	CDL	CB7-C71-C72-C73
79	1H	101	PC7	O11-C11-O3-C3
75	h	203	CDL	C12-C13-C14-C15
75	u	603	CDL	OB6-CB4-CB6-OB8
75	y	202	CDL	OA6-CA4-CA6-OA8
79	T	503	PC7	O2-C2-C3-O3
76	R	401	3PH	O32-C31-O31-C3
75	h	203	CDL	C15-C16-C17-C18
75	1F	401	CDL	C55-C56-C57-C58
75	1K	101	CDL	C76-C77-C78-C79
75	u	603	CDL	C39-C40-C41-C42
75	R	405	CDL	CA7-C31-C32-C33
76	S	301	3PH	C21-C22-C23-C24
77	1E	403	PTY	C8-C11-C12-C13
79	1H	101	PC7	C31-C32-C33-C34
79	T	503	PC7	C11-C12-C13-C14
75	1L	101	CDL	OA9-CA7-OA8-CA6
74	1B	403	HEM	C2A-CAA-CBA-CGA
82	3A	602	HEA	C2A-CAA-CBA-CGA
75	V	603	CDL	CB7-C71-C72-C73
75	h	203	CDL	CA7-C31-C32-C33
76	c	101	3PH	C31-C32-C33-C34
77	S	302	PTY	C30-C31-C32-C33
81	l	701	PGT	C31-C32-C33-C34
77	V	605	PTY	C13-C14-C15-C16
75	1K	101	CDL	C52-C53-C54-C55
81	b	601	PGT	O5-C5-C6-O6
75	1B	408	CDL	CA7-C31-C32-C33
75	1E	401	CDL	CB7-C71-C72-C73
75	R	405	CDL	CB7-C71-C72-C73
75	V	603	CDL	CA7-C31-C32-C33
75	W	701	CDL	CB5-C51-C52-C53
75	u	602	CDL	CB7-C71-C72-C73
75	x	101	CDL	CB5-C51-C52-C53
75	y	202	CDL	CB7-C71-C72-C73
77	R	404	PTY	C30-C31-C32-C33
77	x	102	PTY	C8-C11-C12-C13
79	u	601	PC7	C31-C32-C33-C34
75	W	701	CDL	C74-C75-C76-C77
75	x	101	CDL	C13-C14-C15-C16
79	Q	302	PC7	C4-C5-N-C8

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Mol	Chain	Res	Type	Atoms
75	1B	405	CDL	CB5-C51-C52-C53
75	1M	501	CDL	CB5-C51-C52-C53
75	u	603	CDL	CB7-C71-C72-C73
77	V	605	PTY	C30-C31-C32-C33
76	R	401	3PH	C22-C21-O21-C2
75	1K	101	CDL	C33-C34-C35-C36
75	x	101	CDL	OA9-CA7-OA8-CA6
73	1A	401	UQ5	C14-C16-C17-C18
73	1A	402	UQ5	C9-C11-C12-C13
82	2A	603	HEA	C19-C20-C21-C22
77	V	605	PTY	C19-C20-C21-C22
75	1B	408	CDL	O1-C1-CB2-OB2
75	W	701	CDL	O1-C1-CB2-OB2
81	T	505	PGT	O4P-C4-C5-O5
76	2I	201	3PH	O22-C21-O21-C2
76	S	301	3PH	O22-C21-O21-C2
76	1K	102	3PH	O32-C31-O31-C3
75	u	603	CDL	CA7-C31-C32-C33
76	1E	402	3PH	O32-C31-O31-C3
75	1F	401	CDL	C11-CA5-OA6-CA4
75	u	603	CDL	C11-CA5-OA6-CA4
79	1G	301	PC7	C32-C31-O2-C2
75	1A	405	CDL	CA3-OA5-PA1-OA2
75	1B	405	CDL	CA3-OA5-PA1-OA2
75	1B	405	CDL	CB2-OB2-PB2-OB5
75	1B	405	CDL	CB3-OB5-PB2-OB2
75	1B	408	CDL	CA3-OA5-PA1-OA2
75	1E	401	CDL	CA2-OA2-PA1-OA5
75	1E	401	CDL	CB2-OB2-PB2-OB5
75	1E	401	CDL	CB3-OB5-PB2-OB2
75	1K	101	CDL	CB2-OB2-PB2-OB5
75	1K	101	CDL	CB3-OB5-PB2-OB2
75	1L	101	CDL	CA2-OA2-PA1-OA5
75	1L	101	CDL	CA3-OA5-PA1-OA2
75	1L	101	CDL	CB2-OB2-PB2-OB5
75	1M	501	CDL	CB3-OB5-PB2-OB2
75	R	405	CDL	CA2-OA2-PA1-OA5
75	V	603	CDL	CB2-OB2-PB2-OB5
75	V	603	CDL	CB3-OB5-PB2-OB2
75	W	701	CDL	CA2-OA2-PA1-OA5
75	W	701	CDL	CB3-OB5-PB2-OB2
75	h	203	CDL	CA3-OA5-PA1-OA2

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Mol	Chain	Res	Type	Atoms
75	h	203	CDL	CB3-OB5-PB2-OB2
75	u	602	CDL	CB2-OB2-PB2-OB5
75	u	603	CDL	CA2-OA2-PA1-OA5
75	u	603	CDL	CB2-OB2-PB2-OB5
75	u	603	CDL	CB3-OB5-PB2-OB2
75	x	101	CDL	CA3-OA5-PA1-OA2
75	y	202	CDL	CA3-OA5-PA1-OA2
75	y	202	CDL	CB2-OB2-PB2-OB5
77	1E	403	PTY	C3-O11-P1-O14
77	1F	403	PTY	C3-O11-P1-O14
77	2F	101	PTY	C3-O11-P1-O14
77	R	402	PTY	C3-O11-P1-O14
77	R	402	PTY	C5-O14-P1-O11
77	R	404	PTY	C5-O14-P1-O11
77	S	302	PTY	C3-O11-P1-O14
77	T	501	PTY	C3-O11-P1-O14
77	T	504	PTY	C5-O14-P1-O11
77	T	506	PTY	C3-O11-P1-O14
77	V	604	PTY	C3-O11-P1-O14
77	V	604	PTY	C5-O14-P1-O11
77	V	605	PTY	C5-O14-P1-O11
77	e	302	PTY	C5-O14-P1-O11
77	h	202	PTY	C5-O14-P1-O11
79	1G	301	PC7	C4-O4P-P-O3P
79	1H	101	PC7	C4-O4P-P-O3P
79	2A	606	PC7	C4-O4P-P-O3P
79	u	601	PC7	C4-O4P-P-O3P
81	T	502	PGT	C4-O4P-P-O3P
81	b	601	PGT	C1-O3P-P-O4P
81	l	701	PGT	C4-O4P-P-O3P
75	W	701	CDL	C18-C19-C20-C21
76	w	201	3PH	C21-C22-C23-C24
75	1A	405	CDL	CA2-C1-CB2-OB2
75	1B	405	CDL	CB2-C1-CA2-OA2
75	1B	408	CDL	CA2-C1-CB2-OB2
75	1E	401	CDL	CA2-C1-CB2-OB2
75	x	101	CDL	CA2-C1-CB2-OB2
81	T	505	PGT	O4P-C4-C5-C6
75	1A	405	CDL	OA7-CA5-OA6-CA4
75	1F	401	CDL	OA7-CA5-OA6-CA4
75	u	603	CDL	OA7-CA5-OA6-CA4
76	R	401	3PH	O22-C21-O21-C2

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Mol	Chain	Res	Type	Atoms
76	w	201	3PH	C32-C31-O31-C3
75	1B	405	CDL	C32-C33-C34-C35
75	u	603	CDL	C20-C21-C22-C23
75	u	603	CDL	C31-C32-C33-C34
75	u	603	CDL	C36-C37-C38-C39
75	x	101	CDL	C77-C78-C79-C80
76	V	602	3PH	C26-C27-C28-C29
81	T	502	PGT	C14-C15-C16-C17
76	1R	201	3PH	C22-C21-O21-C2
77	V	605	PTY	C11-C8-O7-C6
81	3A	601	PGT	C32-C31-O2-C2
81	T	505	PGT	C32-C31-O2-C2
75	1K	101	CDL	C81-C82-C83-C84
75	W	701	CDL	C83-C84-C85-C86
75	h	203	CDL	C19-C20-C21-C22
75	u	602	CDL	C36-C37-C38-C39
75	u	603	CDL	C14-C15-C16-C17
75	u	603	CDL	C33-C34-C35-C36
77	S	302	PTY	C11-C12-C13-C14
77	e	302	PTY	C34-C35-C36-C37
89	J	200	8Q1	O27-C28-C29-C30
89	J	200	8Q1	O27-C28-C29-C31
91	s	401	COO	C15-C11-C12-O6A
75	1A	405	CDL	C32-C33-C34-C35
75	1L	101	CDL	C51-C52-C53-C54
75	R	405	CDL	C72-C73-C74-C75
75	W	701	CDL	C77-C78-C79-C80
75	x	101	CDL	C23-C24-C25-C26
76	2I	201	3PH	C24-C25-C26-C27
77	T	501	PTY	C37-C38-C39-C40
79	T	503	PC7	C32-C33-C34-C35
79	1G	301	PC7	O31-C31-O2-C2
81	3A	601	PGT	O31-C31-O2-C2
75	1K	101	CDL	C57-C58-C59-C60
75	1L	101	CDL	C11-C12-C13-C14
75	W	701	CDL	C61-C62-C63-C64
76	V	601	3PH	C2C-C2D-C2E-C2F
75	1B	408	CDL	C1-CA2-OA2-PA1
75	1B	408	CDL	C51-C52-C53-C54
75	1B	408	CDL	C72-C73-C74-C75
75	W	701	CDL	C34-C35-C36-C37
75	h	203	CDL	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
75	h	203	CDL	C72-C73-C74-C75
75	u	603	CDL	C12-C13-C14-C15
75	y	202	CDL	C72-C73-C74-C75
76	1K	102	3PH	C36-C37-C38-C39
76	g	101	3PH	C3E-C3F-C3G-C3H
77	3F	101	PTY	C35-C36-C37-C38
77	V	605	PTY	C32-C33-C34-C35
77	V	606	PTY	C13-C14-C15-C16
81	b	601	PGT	C37-C38-C39-C40
81	l	701	PGT	C39-C40-C41-C42
75	1K	101	CDL	O1-C1-CB2-OB2
75	1K	101	CDL	C32-C33-C34-C35
75	R	405	CDL	C11-C12-C13-C14
75	u	603	CDL	C40-C41-C42-C43
76	h	201	3PH	C2A-C2B-C2C-C2D
77	S	302	PTY	C33-C34-C35-C36
79	1H	101	PC7	C18-C19-C20-C21
81	b	601	PGT	C36-C37-C38-C39
89	r	200	8Q1	C12-C13-C14-C15
77	R	402	PTY	C8-C11-C12-C13
77	e	302	PTY	C30-C31-C32-C33
75	W	701	CDL	C72-C73-C74-C75
75	u	602	CDL	C57-C58-C59-C60
79	T	503	PC7	C13-C14-C15-C16
73	1A	401	UQ5	C20-C19-C21-C22
73	1A	402	UQ5	C25-C24-C26-C27
75	W	701	CDL	C51-C52-C53-C54
75	W	701	CDL	C59-C60-C61-C62
75	u	602	CDL	C62-C63-C64-C65
76	1B	406	3PH	C38-C39-C3A-C3B
76	3I	201	3PH	C29-C2A-C2B-C2C
76	S	301	3PH	C37-C38-C39-C3A
77	x	102	PTY	C16-C17-C18-C19
79	T	503	PC7	C33-C34-C35-C36
73	1B	401	UQ5	C13-C14-C16-C17
75	1L	101	CDL	CA5-C11-C12-C13
75	u	603	CDL	CA5-C11-C12-C13
81	2A	601	PGT	C11-C12-C13-C14
75	1B	408	CDL	C32-C33-C34-C35
75	R	405	CDL	C75-C76-C77-C78
75	W	701	CDL	C35-C36-C37-C38
76	1R	201	3PH	C33-C34-C35-C36

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Mol	Chain	Res	Type	Atoms
76	3D	302	3PH	C25-C26-C27-C28
75	h	203	CDL	C20-C21-C22-C23
75	u	602	CDL	C63-C64-C65-C66
75	u	603	CDL	C16-C17-C18-C19
75	u	603	CDL	C38-C39-C40-C41
75	u	603	CDL	C42-C43-C44-C45
75	x	101	CDL	C79-C80-C81-C82
77	T	504	PTY	C32-C33-C34-C35
81	3A	601	PGT	C4-C5-C6-O6
81	T	502	PGT	C4-C5-C6-O6
81	b	601	PGT	C4-C5-C6-O6
81	l	701	PGT	C4-C5-C6-O6
76	1R	201	3PH	O22-C21-O21-C2
77	V	605	PTY	O10-C8-O7-C6
81	T	505	PGT	O31-C31-O2-C2
81	l	701	PGT	O31-C31-O2-C2
81	l	701	PGT	C32-C31-O2-C2
75	1B	408	CDL	C52-C53-C54-C55
75	V	603	CDL	C71-C72-C73-C74
75	W	701	CDL	C32-C33-C34-C35
75	h	203	CDL	C73-C74-C75-C76
75	x	101	CDL	C16-C17-C18-C19
76	V	602	3PH	C2B-C2C-C2D-C2E
75	1A	405	CDL	CB5-C51-C52-C53
75	1F	401	CDL	CA5-C11-C12-C13
76	g	101	3PH	C21-C22-C23-C24
81	3A	601	PGT	C11-C12-C13-C14
75	1K	101	CDL	C72-C73-C74-C75
75	1L	101	CDL	C52-C53-C54-C55
75	h	203	CDL	C57-C58-C59-C60
75	x	101	CDL	C21-C22-C23-C24
76	1B	406	3PH	C34-C35-C36-C37
76	c	101	3PH	C33-C34-C35-C36
76	y	201	3PH	C37-C38-C39-C3A
77	V	605	PTY	C33-C34-C35-C36
77	x	102	PTY	C22-C23-C24-C25
79	Q	302	PC7	C12-C13-C14-C15
79	T	503	PC7	C40-C41-C42-C43
81	T	505	PGT	C32-C33-C34-C35
81	T	505	PGT	C19-C20-C21-C22
89	r	200	8Q1	C11-C10-C9-C8
75	1K	101	CDL	C75-C76-C77-C78

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Mol	Chain	Res	Type	Atoms
75	x	101	CDL	C15-C16-C17-C18
76	2I	201	3PH	C29-C2A-C2B-C2C
81	b	601	PGT	C16-C17-C18-C19
77	1E	403	PTY	N1-C2-C3-O11
77	2F	101	PTY	N1-C2-C3-O11
75	1K	101	CDL	C11-C12-C13-C14
75	W	701	CDL	C11-C12-C13-C14
75	h	203	CDL	C32-C33-C34-C35
76	c	101	3PH	C35-C36-C37-C38
81	3A	601	PGT	C15-C16-C17-C18
81	b	601	PGT	C32-C33-C34-C35
76	w	201	3PH	O32-C31-O31-C3
75	1A	405	CDL	C52-C53-C54-C55
75	h	203	CDL	C31-C32-C33-C34
75	h	203	CDL	C80-C81-C82-C83
77	R	404	PTY	C25-C26-C27-C28
77	S	302	PTY	C37-C38-C39-C40
79	T	503	PC7	C39-C40-C41-C42
81	T	502	PGT	C16-C17-C18-C19
75	1E	401	CDL	C31-CA7-OA8-CA6
75	V	603	CDL	C11-C12-C13-C14
75	x	101	CDL	C11-C12-C13-C14
91	s	401	COO	N2-C5-C6-S1
75	1B	408	CDL	C73-C74-C75-C76
75	V	603	CDL	C13-C14-C15-C16
75	x	101	CDL	C62-C63-C64-C65
75	x	101	CDL	C63-C64-C65-C66
77	T	506	PTY	C12-C13-C14-C15
77	e	302	PTY	C13-C14-C15-C16
79	T	503	PC7	C38-C39-C40-C41
75	1L	101	CDL	C74-C75-C76-C77
75	V	603	CDL	C34-C35-C36-C37
75	u	602	CDL	C16-C17-C18-C19
75	x	101	CDL	C57-C58-C59-C60
76	1E	402	3PH	C2B-C2C-C2D-C2E
76	g	101	3PH	C37-C38-C39-C3A
75	1B	408	CDL	C71-C72-C73-C74
81	b	601	PGT	C17-C18-C19-C20
79	Q	302	PC7	C11-C12-C13-C14
75	1F	401	CDL	C51-C52-C53-C54
75	x	101	CDL	C54-C55-C56-C57
79	T	503	PC7	C17-C18-C19-C20

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Mol	Chain	Res	Type	Atoms
73	1A	401	UQ5	C18-C19-C21-C22
75	h	203	CDL	C11-CA5-OA6-CA4
75	h	203	CDL	C51-CB5-OB6-CB4
77	2F	101	PTY	C11-C8-O7-C6
79	3A	606	PC7	C32-C31-O2-C2
76	1A	406	3PH	C2A-C2B-C2C-C2D
75	W	701	CDL	C17-C18-C19-C20
77	R	406	PTY	C14-C15-C16-C17
79	3A	606	PC7	C11-C12-C13-C14
75	1B	405	CDL	O1-C1-CB2-OB2
81	T	505	PGT	C18-C19-C20-C21
75	1B	408	CDL	C16-C17-C18-C19
75	u	603	CDL	C34-C35-C36-C37
75	h	203	CDL	OA7-CA5-OA6-CA4
75	h	203	CDL	OB7-CB5-OB6-CB4
76	w	201	3PH	O22-C21-O21-C2
77	2F	101	PTY	O10-C8-O7-C6
79	3A	606	PC7	O31-C31-O2-C2
75	x	101	CDL	C80-C81-C82-C83
76	R	401	3PH	C36-C37-C38-C39
77	1F	403	PTY	C34-C35-C36-C37
76	1B	406	3PH	C33-C34-C35-C36
77	2F	101	PTY	C34-C35-C36-C37
75	1L	101	CDL	CB7-C71-C72-C73
75	1M	501	CDL	CA5-C11-C12-C13
75	W	701	CDL	C62-C63-C64-C65
75	W	701	CDL	C76-C77-C78-C79
75	W	701	CDL	C81-C82-C83-C84
76	1K	102	3PH	C23-C24-C25-C26
76	h	201	3PH	C33-C34-C35-C36
77	T	504	PTY	C11-C8-O7-C6
75	W	701	CDL	C14-C15-C16-C17
76	w	201	3PH	C38-C39-C3A-C3B
77	R	404	PTY	C24-C25-C26-C27
81	T	505	PGT	C15-C16-C17-C18
81	l	701	PGT	C11-C12-C13-C14
77	1F	403	PTY	C31-C32-C33-C34
77	T	501	PTY	C19-C20-C21-C22
79	T	503	PC7	C44-C45-C46-C47
73	1A	401	UQ5	C13-C14-C16-C17
73	1A	402	UQ5	C23-C24-C26-C27
75	1E	401	CDL	OA9-CA7-OA8-CA6

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Mol	Chain	Res	Type	Atoms
75	y	202	CDL	OB7-CB5-OB6-CB4
76	1K	102	3PH	O22-C21-O21-C2
75	u	603	CDL	C71-CB7-OB8-CB6
76	2D	302	3PH	C32-C31-O31-C3
76	y	201	3PH	C32-C31-O31-C3
75	1M	501	CDL	C32-C33-C34-C35
75	u	603	CDL	C71-C72-C73-C74
91	s	401	COO	O4-C7-C8-C9
75	1L	101	CDL	C72-C73-C74-C75
77	V	604	PTY	C34-C35-C36-C37
79	T	503	PC7	C15-C16-C17-C18
75	1M	501	CDL	C33-C34-C35-C36
75	W	701	CDL	C80-C81-C82-C83
75	u	602	CDL	C13-C14-C15-C16
75	u	602	CDL	C33-C34-C35-C36
81	l	701	PGT	C40-C41-C42-C43
89	J	200	8Q1	C10-C11-C12-C13
77	T	501	PTY	C6-C1-O4-C30
75	1K	101	CDL	C13-C14-C15-C16
73	1B	401	UQ5	C24-C26-C27-C28
75	1F	401	CDL	C54-C55-C56-C57
75	u	602	CDL	C54-C55-C56-C57
79	u	601	PC7	C39-C40-C41-C42
75	R	405	CDL	C11-CA5-OA6-CA4
75	u	602	CDL	C11-CA5-OA6-CA4
75	y	202	CDL	C51-CB5-OB6-CB4
76	1B	406	3PH	C22-C21-O21-C2
76	1K	102	3PH	C22-C21-O21-C2
76	w	201	3PH	C22-C21-O21-C2
79	Q	302	PC7	C32-C31-O2-C2
75	1M	501	CDL	OB5-CB3-CB4-OB6
76	y	201	3PH	O11-C1-C2-O21
76	1A	406	3PH	C24-C25-C26-C27
76	V	602	3PH	C2A-C2B-C2C-C2D
75	x	101	CDL	C55-C56-C57-C58
77	T	504	PTY	O10-C8-O7-C6
79	Q	302	PC7	O31-C31-O2-C2
76	2D	302	3PH	O21-C2-C3-O31
77	R	402	PTY	O4-C1-C6-O7
77	T	506	PTY	O4-C1-C6-O7
75	1F	401	CDL	C11-C12-C13-C14
75	1K	101	CDL	C78-C79-C80-C81

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Mol	Chain	Res	Type	Atoms
75	R	405	CDL	C32-C33-C34-C35
77	R	404	PTY	C16-C17-C18-C19
79	Q	302	PC7	C4-C5-N-C6
75	1B	408	CDL	C11-C12-C13-C14
75	1B	408	CDL	C36-C37-C38-C39
75	V	603	CDL	C33-C34-C35-C36
73	1A	401	UQ5	C15-C14-C16-C17
75	1A	405	CDL	C15-C16-C17-C18
75	x	101	CDL	C51-C52-C53-C54
75	1A	405	CDL	C34-C35-C36-C37
76	2D	302	3PH	C23-C24-C25-C26
76	3I	201	3PH	C32-C33-C34-C35
77	x	102	PTY	C20-C21-C22-C23
76	1B	406	3PH	O22-C21-O21-C2
75	V	603	CDL	C51-CB5-OB6-CB4
75	x	101	CDL	C60-C61-C62-C63
75	x	101	CDL	C83-C84-C85-C86
75	1A	405	CDL	CB3-OB5-PB2-OB2
75	u	603	CDL	CA3-OA5-PA1-OA2
77	T	506	PTY	C5-O14-P1-O11
77	V	605	PTY	C3-O11-P1-O14
79	1H	101	PC7	C1-O3P-P-O4P
79	3A	606	PC7	C4-O4P-P-O3P
75	1L	101	CDL	C75-C76-C77-C78
75	u	603	CDL	C15-C16-C17-C18
76	h	201	3PH	C36-C37-C38-C39
77	T	504	PTY	C30-C31-C32-C33
75	1B	408	CDL	CB4-CB3-OB5-PB2
75	h	203	CDL	CB4-CB3-OB5-PB2
77	V	605	PTY	C6-C5-O14-P1
75	h	203	CDL	C16-C17-C18-C19
76	2D	302	3PH	C22-C23-C24-C25
81	T	502	PGT	C36-C37-C38-C39
75	x	101	CDL	C71-CB7-OB8-CB6
77	3D	301	PTY	C31-C30-O4-C1
76	3D	302	3PH	O11-C1-C2-C3
76	V	601	3PH	O11-C1-C2-C3
76	c	101	3PH	O11-C1-C2-C3
76	h	201	3PH	O11-C1-C2-C3
81	l	701	PGT	O3P-C1-C2-C3
75	u	602	CDL	C11-C12-C13-C14
75	x	101	CDL	C19-C20-C21-C22

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Mol	Chain	Res	Type	Atoms
79	1H	101	PC7	C12-C13-C14-C15
75	1A	405	CDL	CA5-C11-C12-C13
75	u	602	CDL	C18-C19-C20-C21
76	1E	402	3PH	C28-C29-C2A-C2B
76	1K	102	3PH	C27-C28-C29-C2A
75	1F	401	CDL	C12-C13-C14-C15
77	T	501	PTY	C21-C22-C23-C24
75	x	101	CDL	C12-C13-C14-C15
76	1A	406	3PH	C23-C24-C25-C26
76	3I	201	3PH	C36-C37-C38-C39
76	V	602	3PH	C34-C35-C36-C37
76	w	201	3PH	C2A-C2B-C2C-C2D
77	e	302	PTY	C31-C32-C33-C34
79	T	503	PC7	C42-C43-C44-C45
75	1K	101	CDL	CA2-C1-CB2-OB2
75	W	701	CDL	CB2-C1-CA2-OA2
75	u	602	CDL	OA7-CA5-OA6-CA4
75	1B	405	CDL	C52-C53-C54-C55
75	x	101	CDL	C74-C75-C76-C77
75	V	603	CDL	C21-C22-C23-C24
77	e	302	PTY	C8-C11-C12-C13
76	1B	407	3PH	C22-C21-O21-C2
75	u	603	CDL	OB9-CB7-OB8-CB6
76	y	201	3PH	O32-C31-O31-C3
76	3D	302	3PH	C24-C25-C26-C27
77	R	404	PTY	C33-C34-C35-C36
75	1B	405	CDL	CB3-CB4-CB6-OB8
75	1B	408	CDL	CA3-CA4-CA6-OA8
75	1K	101	CDL	CA3-CA4-CA6-OA8
75	1K	101	CDL	CB3-CB4-CB6-OB8
75	R	405	CDL	C77-C78-C79-C80
75	V	603	CDL	C32-C33-C34-C35
75	h	203	CDL	CB3-CB4-CB6-OB8
75	h	203	CDL	C76-C77-C78-C79
75	u	603	CDL	CB3-CB4-CB6-OB8
75	x	101	CDL	CA3-CA4-CA6-OA8
75	y	202	CDL	CA3-CA4-CA6-OA8
76	1B	406	3PH	C1-C2-C3-O31
76	1E	402	3PH	C1-C2-C3-O31
76	2D	302	3PH	C1-C2-C3-O31
77	1E	403	PTY	O4-C1-C6-C5
77	3F	101	PTY	O4-C1-C6-C5

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Mol	Chain	Res	Type	Atoms
77	R	404	PTY	O4-C1-C6-C5
81	2A	601	PGT	C1-C2-C3-O3
81	l	701	PGT	C41-C42-C43-C44
76	1E	402	3PH	C25-C26-C27-C28
77	R	402	PTY	C13-C14-C15-C16
75	u	603	CDL	C37-C38-C39-C40
75	1B	405	CDL	C11-C12-C13-C14
75	1B	408	CDL	C74-C75-C76-C77
75	V	603	CDL	C23-C24-C25-C26
75	u	603	CDL	C44-C45-C46-C47
77	2D	301	PTY	C17-C18-C19-C20
75	x	101	CDL	CB7-C71-C72-C73
76	1B	407	3PH	C21-C22-C23-C24
79	2A	606	PC7	C31-C32-C33-C34
76	2D	302	3PH	O32-C31-O31-C3
75	1K	101	CDL	C59-C60-C61-C62
77	1F	403	PTY	C11-C12-C13-C14
79	1H	101	PC7	C13-C14-C15-C16
89	r	200	8Q1	O33-C32-C34-O35
75	u	602	CDL	C37-C38-C39-C40
75	u	602	CDL	C61-C62-C63-C64
77	V	605	PTY	C35-C36-C37-C38
75	1B	405	CDL	C76-C77-C78-C79
76	1A	406	3PH	C29-C2A-C2B-C2C
76	1B	406	3PH	C27-C28-C29-C2A
76	V	601	3PH	C37-C38-C39-C3A
75	1M	501	CDL	CB7-C71-C72-C73
75	1B	405	CDL	CA7-C31-C32-C33
77	1E	403	PTY	C32-C33-C34-C35
77	T	501	PTY	C32-C33-C34-C35
79	T	503	PC7	C45-C46-C47-C48
75	1B	405	CDL	C84-C85-C86-C87
75	1K	101	CDL	C73-C74-C75-C76
77	G	303	PTY	C8-C11-C12-C13
77	T	506	PTY	C31-C30-O4-C1
75	1B	408	CDL	C18-C19-C20-C21
75	1L	101	CDL	C76-C77-C78-C79
77	e	302	PTY	C17-C18-C19-C20
81	T	502	PGT	C20-C21-C22-C23
75	1E	401	CDL	C11-C12-C13-C14
75	W	701	CDL	C19-C20-C21-C22
75	x	101	CDL	C36-C37-C38-C39

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Mol	Chain	Res	Type	Atoms
79	T	503	PC7	C23-C24-C25-C26
75	W	701	CDL	CB6-CB4-OB6-CB5
75	R	405	CDL	OA7-CA5-OA6-CA4
75	u	602	CDL	C74-C75-C76-C77
76	2I	201	3PH	C1-O11-P-O12
76	h	201	3PH	C1-O11-P-O12
79	R	403	PC7	C2-C1-O3P-P
75	1B	408	CDL	C37-C38-C39-C40
75	W	701	CDL	C54-C55-C56-C57
75	W	701	CDL	C75-C76-C77-C78
77	T	501	PTY	C31-C30-O4-C1
75	1A	405	CDL	OA5-CA3-CA4-OA6
77	3D	301	PTY	O14-C5-C6-O7
77	S	302	PTY	O14-C5-C6-O7
77	V	605	PTY	C12-C11-C8-O7
81	b	601	PGT	C11-C12-C13-C14
81	b	601	PGT	C18-C19-C20-C21
77	3D	301	PTY	O30-C30-O4-C1
76	g	101	3PH	C38-C39-C3A-C3B
77	V	605	PTY	C39-C40-C41-C42
75	u	603	CDL	C51-C52-C53-C54
76	1B	406	3PH	O21-C2-C3-O31
77	S	302	PTY	O4-C1-C6-O7
75	1M	501	CDL	C51-C52-C53-C54
76	1R	201	3PH	C2D-C2E-C2F-C2G
75	x	101	CDL	OB9-CB7-OB8-CB6
77	S	302	PTY	C8-C11-C12-C13
75	1L	101	CDL	C12-C13-C14-C15
75	x	101	CDL	C32-C33-C34-C35
75	x	101	CDL	C61-C62-C63-C64
75	y	202	CDL	C12-C13-C14-C15
76	h	201	3PH	C3D-C3E-C3F-C3G
91	s	401	COO	P1A-O3A-P2A-O4A
75	1M	501	CDL	C37-C38-C39-C40
75	1M	501	CDL	C52-C53-C54-C55
75	y	202	CDL	C73-C74-C75-C76
76	S	301	3PH	C32-C33-C34-C35
75	R	405	CDL	C12-C13-C14-C15
76	S	301	3PH	C38-C39-C3A-C3B
76	S	301	3PH	C39-C3A-C3B-C3C
75	1B	408	CDL	C12-C13-C14-C15
75	1L	101	CDL	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
75	V	603	CDL	C19-C20-C21-C22
77	2D	301	PTY	C19-C20-C21-C22
75	W	701	CDL	C31-CA7-OA8-CA6
77	1F	403	PTY	C31-C30-O4-C1
81	3A	601	PGT	C12-C11-O3-C3
75	1F	401	CDL	C32-C33-C34-C35
76	1K	102	3PH	C35-C36-C37-C38
79	Q	302	PC7	C14-C15-C16-C17
76	1B	407	3PH	C37-C38-C39-C3A
75	1F	401	CDL	C71-C72-C73-C74
75	h	203	CDL	C56-C57-C58-C59
75	1B	408	CDL	OA5-CA3-CA4-CA6
75	1E	401	CDL	OB5-CB3-CB4-CB6
75	1F	401	CDL	OB5-CB3-CB4-CB6
75	1M	501	CDL	OA5-CA3-CA4-CA6
75	1M	501	CDL	OB5-CB3-CB4-CB6
75	R	405	CDL	OB5-CB3-CB4-CB6
75	V	603	CDL	OA5-CA3-CA4-CA6
75	y	202	CDL	OB5-CB3-CB4-CB6
77	3D	301	PTY	O14-C5-C6-C1
77	R	404	PTY	O14-C5-C6-C1
77	R	406	PTY	O14-C5-C6-C1
77	e	302	PTY	O14-C5-C6-C1
75	1B	405	CDL	C81-C82-C83-C84
75	1B	405	CDL	CB7-C71-C72-C73
75	1L	101	CDL	CB5-C51-C52-C53
75	1K	101	CDL	C83-C84-C85-C86
75	W	701	CDL	C40-C41-C42-C43
79	3A	606	PC7	C32-C33-C34-C35
75	u	602	CDL	C71-CB7-OB8-CB6
75	x	101	CDL	C18-C19-C20-C21
76	h	201	3PH	C26-C27-C28-C29
75	x	101	CDL	C56-C57-C58-C59
81	T	502	PGT	C18-C19-C20-C21
75	1E	401	CDL	O1-C1-CA2-OA2
75	V	603	CDL	OB7-CB5-OB6-CB4
75	W	701	CDL	C52-C53-C54-C55
75	W	701	CDL	C82-C83-C84-C85
76	V	601	3PH	C2B-C2C-C2D-C2E
75	1M	501	CDL	C11-CA5-OA6-CA4
75	1K	101	CDL	C71-C72-C73-C74
77	e	302	PTY	C39-C40-C41-C42

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Mol	Chain	Res	Type	Atoms
81	l	701	PGT	C34-C35-C36-C37
75	1L	101	CDL	C1-CB2-OB2-PB2
75	u	603	CDL	CA4-CA3-OA5-PA1
76	2I	201	3PH	C2-C1-O11-P
79	2A	606	PC7	C2-C1-O3P-P
74	1A	403	HEM	C2A-CAA-CBA-CGA
75	h	203	CDL	C33-C34-C35-C36
77	h	202	PTY	C31-C32-C33-C34
75	h	203	CDL	C77-C78-C79-C80
77	V	604	PTY	C37-C38-C39-C40
75	1B	405	CDL	C71-CB7-OB8-CB6
75	1F	401	CDL	CB3-CB4-CB6-OB8
75	1L	101	CDL	CA3-CA4-CA6-OA8
75	V	603	CDL	CA3-CA4-CA6-OA8
75	h	203	CDL	CA3-CA4-CA6-OA8
75	y	202	CDL	CB3-CB4-CB6-OB8
76	1R	201	3PH	C1-C2-C3-O31
77	1F	403	PTY	O4-C1-C6-C5
77	3D	301	PTY	O4-C1-C6-C5
77	R	402	PTY	O4-C1-C6-C5
77	S	302	PTY	O4-C1-C6-C5
77	T	506	PTY	O4-C1-C6-C5
77	V	604	PTY	O4-C1-C6-C5
79	T	503	PC7	C1-C2-C3-O3
81	T	505	PGT	C1-C2-C3-O3
75	V	603	CDL	C14-C15-C16-C17
77	S	302	PTY	C12-C13-C14-C15
77	T	501	PTY	O30-C30-O4-C1
77	T	506	PTY	O30-C30-O4-C1
76	w	201	3PH	C3C-C3D-C3E-C3F
75	W	701	CDL	C60-C61-C62-C63
77	2D	301	PTY	C16-C17-C18-C19
77	V	606	PTY	C14-C15-C16-C17
81	T	505	PGT	C14-C15-C16-C17
75	1K	101	CDL	C34-C35-C36-C37
76	2I	201	3PH	C26-C27-C28-C29
75	1E	401	CDL	C31-C32-C33-C34
77	1E	403	PTY	C31-C32-C33-C34
79	T	503	PC7	C16-C17-C18-C19
75	1M	501	CDL	CA3-OA5-PA1-OA2
75	x	101	CDL	CB3-OB5-PB2-OB2
77	S	302	PTY	C5-O14-P1-O11

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Mol	Chain	Res	Type	Atoms
76	1E	402	3PH	C27-C28-C29-C2A
75	1B	405	CDL	C31-C32-C33-C34
75	1B	408	CDL	C17-C18-C19-C20
76	1B	406	3PH	O11-C1-C2-O21
77	T	504	PTY	O14-C5-C6-O7
79	1G	301	PC7	O3P-C1-C2-O2
77	3D	301	PTY	C30-C31-C32-C33
79	u	601	PC7	C16-C17-C18-C19
75	V	603	CDL	O1-C1-CA2-OA2
75	u	602	CDL	C22-C23-C24-C25
77	R	404	PTY	C23-C24-C25-C26
76	c	101	3PH	C22-C23-C24-C25
77	S	302	PTY	C13-C14-C15-C16
77	S	302	PTY	C38-C39-C40-C41
75	1F	401	CDL	OB6-CB4-CB6-OB8
75	1K	101	CDL	OB6-CB4-CB6-OB8
75	y	202	CDL	OB6-CB4-CB6-OB8
76	1B	407	3PH	O21-C2-C3-O31
76	h	201	3PH	O21-C2-C3-O31
77	V	604	PTY	O4-C1-C6-O7
79	1H	101	PC7	O2-C2-C3-O3
79	R	403	PC7	O2-C2-C3-O3
79	u	601	PC7	O2-C2-C3-O3
81	T	505	PGT	O2-C2-C3-O3
81	b	601	PGT	O2-C2-C3-O3
81	T	502	PGT	O2-C31-C32-C33
79	u	601	PC7	C32-C33-C34-C35
75	1K	101	CDL	C11-CA5-OA6-CA4
75	h	203	CDL	CA5-C11-C12-C13
73	1A	402	UQ5	C24-C26-C27-C28
75	1K	101	CDL	CB2-C1-CA2-OA2
75	R	405	CDL	CB2-C1-CA2-OA2
75	u	603	CDL	CB2-C1-CA2-OA2
75	1M	501	CDL	C11-C12-C13-C14
77	x	102	PTY	C26-C27-C28-C29
81	l	701	PGT	C20-C21-C22-C23
75	1M	501	CDL	OA7-CA5-OA6-CA4
75	u	602	CDL	C24-C25-C26-C27
76	1A	406	3PH	C25-C26-C27-C28
75	u	602	CDL	CA5-C11-C12-C13
75	h	203	CDL	C55-C56-C57-C58
77	V	606	PTY	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
75	1A	405	CDL	C51-C52-C53-C54
75	1B	405	CDL	C73-C74-C75-C76
75	u	602	CDL	C51-C52-C53-C54
75	u	603	CDL	C21-C22-C23-C24
75	y	202	CDL	C51-C52-C53-C54
76	1E	402	3PH	C32-C33-C34-C35
75	1A	405	CDL	C1-CA2-OA2-PA1
75	1A	405	CDL	CB4-CB3-OB5-PB2
75	1E	401	CDL	C1-CB2-OB2-PB2
75	1F	401	CDL	CB4-CB3-OB5-PB2
76	R	401	3PH	C2-C1-O11-P
76	y	201	3PH	C2-C1-O11-P
77	V	604	PTY	C6-C5-O14-P1
75	R	405	CDL	C74-C75-C76-C77
77	2F	101	PTY	C35-C36-C37-C38
77	T	501	PTY	C11-C12-C13-C14
79	1H	101	PC7	C4-C5-N-C6
75	1F	401	CDL	C31-C32-C33-C34
76	1B	407	3PH	C2D-C2E-C2F-C2G
77	G	303	PTY	C37-C38-C39-C40
77	R	406	PTY	C39-C40-C41-C42
75	1M	501	CDL	C34-C35-C36-C37
79	2A	606	PC7	C32-C33-C34-C35
75	1F	401	CDL	CB7-C71-C72-C73
77	e	301	PTY	C30-C31-C32-C33
75	1K	101	CDL	OA7-CA5-OA6-CA4
76	1B	407	3PH	O22-C21-O21-C2
77	V	606	PTY	C11-C8-O7-C6
75	1B	405	CDL	C75-C76-C77-C78
75	1A	405	CDL	CB7-C71-C72-C73
90	P	401	NDP	PN-O3-PA-O5B
75	1E	401	CDL	C71-C72-C73-C74
75	1E	401	CDL	C73-C74-C75-C76
75	1K	101	CDL	OA5-CA3-CA4-CA6
75	u	602	CDL	OB5-CB3-CB4-CB6
76	1A	406	3PH	O11-C1-C2-C3
76	1K	102	3PH	O11-C1-C2-C3
76	2D	302	3PH	O11-C1-C2-C3
76	y	201	3PH	O11-C1-C2-C3
77	S	302	PTY	O14-C5-C6-C1
77	T	506	PTY	O14-C5-C6-C1
79	u	601	PC7	O3P-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
81	T	502	PGT	O3P-C1-C2-C3
81	T	505	PGT	O3P-C1-C2-C3
75	1L	101	CDL	O1-C1-CA2-OA2
75	u	602	CDL	C15-C16-C17-C18
75	x	101	CDL	C75-C76-C77-C78
77	T	501	PTY	C33-C34-C35-C36
75	u	602	CDL	C59-C60-C61-C62
89	J	200	8Q1	C7-C8-C9-C10
75	1K	101	CDL	C31-CA7-OA8-CA6
79	Q	302	PC7	C12-C11-O3-C3
76	2D	302	3PH	C28-C29-C2A-C2B
75	u	602	CDL	C20-C21-C22-C23
77	T	501	PTY	C40-C41-C42-C43
89	r	200	8Q1	C28-O27-P24-O2
75	V	603	CDL	C72-C73-C74-C75
77	x	102	PTY	C31-C30-O4-C1
77	G	303	PTY	C32-C33-C34-C35
76	R	401	3PH	C3-C2-O21-C21
76	w	201	3PH	C3-C2-O21-C21
81	l	701	PGT	C3-C2-O2-C31
75	W	701	CDL	C64-C65-C66-C67
76	c	101	3PH	C29-C2A-C2B-C2C
76	g	101	3PH	C32-C33-C34-C35
73	1A	402	UQ5	C12-C11-C9-C10
75	1K	101	CDL	C31-C32-C33-C34
76	R	401	3PH	C26-C27-C28-C29
75	h	203	CDL	C17-C18-C19-C20
75	u	602	CDL	C58-C59-C60-C61
76	1A	406	3PH	C27-C28-C29-C2A
75	1B	408	CDL	CA4-CA3-OA5-PA1
75	1L	101	CDL	CB4-CB3-OB5-PB2
75	1M	501	CDL	CB3-CB4-CB6-OB8
75	R	405	CDL	CB3-CB4-CB6-OB8
76	1B	407	3PH	C1-C2-C3-O31
76	h	201	3PH	C1-C2-C3-O31
79	1H	101	PC7	C1-C2-C3-O3
79	u	601	PC7	C1-C2-C3-O3
81	b	601	PGT	C1-C2-C3-O3
77	1F	403	PTY	O30-C30-O4-C1
75	1B	405	CDL	OB5-CB3-CB4-OB6
75	1B	408	CDL	OA5-CA3-CA4-OA6
75	1E	401	CDL	OB5-CB3-CB4-OB6

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Mol	Chain	Res	Type	Atoms
75	1K	101	CDL	OB5-CB3-CB4-OB6
75	1M	501	CDL	OA5-CA3-CA4-OA6
75	V	603	CDL	OA5-CA3-CA4-OA6
75	h	203	CDL	OB5-CB3-CB4-OB6
76	1E	402	3PH	O11-C1-C2-O21
76	1K	102	3PH	O11-C1-C2-O21
76	3I	201	3PH	O11-C1-C2-O21
76	c	101	3PH	O11-C1-C2-O21
76	w	201	3PH	O11-C1-C2-O21
77	R	404	PTY	O14-C5-C6-O7
77	T	506	PTY	O14-C5-C6-O7
79	u	601	PC7	O3P-C1-C2-O2
76	w	201	3PH	C29-C2A-C2B-C2C
75	1K	101	CDL	OA9-CA7-OA8-CA6
75	y	202	CDL	C11-C12-C13-C14
77	V	606	PTY	O10-C8-O7-C6
75	V	603	CDL	C12-C13-C14-C15
75	W	701	CDL	OA9-CA7-OA8-CA6
81	3A	601	PGT	O11-C11-O3-C3
75	1L	101	CDL	OA6-CA4-CA6-OA8
75	R	405	CDL	OB6-CB4-CB6-OB8
75	V	603	CDL	OA6-CA4-CA6-OA8
75	W	701	CDL	OB6-CB4-CB6-OB8
75	h	203	CDL	OA6-CA4-CA6-OA8
76	1A	406	3PH	O21-C2-C3-O31
76	1R	201	3PH	O21-C2-C3-O31
76	w	201	3PH	O21-C2-C3-O31
77	1E	403	PTY	O4-C1-C6-O7
77	2F	101	PTY	O4-C1-C6-O7
77	3D	301	PTY	O4-C1-C6-O7
77	R	404	PTY	O4-C1-C6-O7
77	R	406	PTY	O4-C1-C6-O7
77	V	605	PTY	O4-C1-C6-O7
77	V	606	PTY	O4-C1-C6-O7
81	l	701	PGT	O2-C2-C3-O3
75	1B	405	CDL	OB9-CB7-OB8-CB6
75	u	602	CDL	OB9-CB7-OB8-CB6
75	1B	405	CDL	C72-C71-CB7-OB8
75	V	603	CDL	C32-C31-CA7-OA8
75	W	701	CDL	C44-C45-C46-C47
75	h	203	CDL	C51-C52-C53-C54
75	h	203	CDL	C78-C79-C80-C81

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Mol	Chain	Res	Type	Atoms
81	T	502	PGT	O5-C5-C6-O6
75	1A	405	CDL	C31-C32-C33-C34
76	1K	102	3PH	C28-C29-C2A-C2B
77	V	604	PTY	C11-C8-O7-C6
77	x	102	PTY	C32-C33-C34-C35
75	W	701	CDL	C71-C72-C73-C74
77	V	604	PTY	O10-C8-O7-C6
77	x	102	PTY	O30-C30-O4-C1
79	Q	302	PC7	O11-C11-O3-C3
75	R	405	CDL	C31-CA7-OA8-CA6
75	1K	101	CDL	C37-C38-C39-C40
75	h	203	CDL	C74-C75-C76-C77
75	x	101	CDL	C84-C85-C86-C87
76	R	401	3PH	C25-C26-C27-C28
79	1G	301	PC7	C12-C11-O3-C3
77	R	404	PTY	C13-C14-C15-C16
77	3D	301	PTY	C3-O11-P1-O14
77	R	404	PTY	C3-O11-P1-O14
77	V	606	PTY	C5-O14-P1-O11
77	e	301	PTY	C5-O14-P1-O11
79	R	403	PC7	C4-O4P-P-O3P
75	V	603	CDL	C35-C36-C37-C38
75	W	701	CDL	C43-C44-C45-C46
73	1A	402	UQ5	C20-C19-C21-C22
75	1M	501	CDL	C1-CB2-OB2-PB2
75	V	603	CDL	C1-CA2-OA2-PA1
75	W	701	CDL	CB4-CB3-OB5-PB2
76	1B	406	3PH	C2-C1-O11-P
77	2D	301	PTY	C6-C5-O14-P1
79	1H	101	PC7	C2-C1-O3P-P
75	1A	405	CDL	CB3-OB5-PB2-OB3
75	1B	405	CDL	CA3-OA5-PA1-OA3
75	1B	405	CDL	CB2-OB2-PB2-OB3
75	1B	405	CDL	CB3-OB5-PB2-OB4
75	1B	408	CDL	CA3-OA5-PA1-OA3
75	1B	408	CDL	CA3-OA5-PA1-OA4
75	1E	401	CDL	CB3-OB5-PB2-OB3
75	1E	401	CDL	CB3-OB5-PB2-OB4
75	1K	101	CDL	CA3-OA5-PA1-OA4
75	1K	101	CDL	CB3-OB5-PB2-OB4
75	1L	101	CDL	CA2-OA2-PA1-OA3
75	1M	501	CDL	CB3-OB5-PB2-OB4

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Mol	Chain	Res	Type	Atoms
75	R	405	CDL	CB3-OB5-PB2-OB4
75	V	603	CDL	CA2-OA2-PA1-OA4
75	V	603	CDL	CA3-OA5-PA1-OA3
75	W	701	CDL	CA2-OA2-PA1-OA4
75	W	701	CDL	CB3-OB5-PB2-OB3
75	h	203	CDL	CB3-OB5-PB2-OB4
75	u	602	CDL	CB2-OB2-PB2-OB3
75	u	602	CDL	CB2-OB2-PB2-OB4
75	u	603	CDL	CA3-OA5-PA1-OA4
75	u	603	CDL	CB2-OB2-PB2-OB3
75	u	603	CDL	CB3-OB5-PB2-OB4
75	x	101	CDL	CA3-OA5-PA1-OA3
75	y	202	CDL	CB2-OB2-PB2-OB3
75	y	202	CDL	CB2-OB2-PB2-OB4
77	1E	403	PTY	C3-O11-P1-O13
77	3D	301	PTY	C3-O11-P1-O12
77	3F	101	PTY	C3-O11-P1-O12
77	3F	101	PTY	C5-O14-P1-O12
77	R	402	PTY	C5-O14-P1-O13
77	R	406	PTY	C5-O14-P1-O12
77	T	501	PTY	C3-O11-P1-O13
77	T	501	PTY	C5-O14-P1-O12
77	T	506	PTY	C3-O11-P1-O13
77	T	506	PTY	C5-O14-P1-O12
77	T	506	PTY	C5-O14-P1-O13
77	V	604	PTY	C5-O14-P1-O13
77	V	605	PTY	C3-O11-P1-O12
77	h	202	PTY	C3-O11-P1-O12
79	1G	301	PC7	C4-O4P-P-O1P
79	1H	101	PC7	C1-O3P-P-O1P
79	1H	101	PC7	C4-O4P-P-O1P
79	2A	606	PC7	C4-O4P-P-O2P
79	3A	606	PC7	C4-O4P-P-O1P
81	3A	601	PGT	C1-O3P-P-O2P
81	T	502	PGT	C4-O4P-P-O2P
81	T	505	PGT	C1-O3P-P-O2P
75	1K	101	CDL	CA7-C31-C32-C33
75	1A	405	CDL	OA5-CA3-CA4-CA6
75	1B	405	CDL	OA5-CA3-CA4-CA6
75	1B	405	CDL	OB5-CB3-CB4-CB6
75	V	603	CDL	OB5-CB3-CB4-CB6
75	h	203	CDL	OA5-CA3-CA4-CA6

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Mol	Chain	Res	Type	Atoms
75	h	203	CDL	OB5-CB3-CB4-CB6
75	y	202	CDL	OA5-CA3-CA4-CA6
76	1B	406	3PH	O11-C1-C2-C3
76	1E	402	3PH	O11-C1-C2-C3
76	1R	201	3PH	O11-C1-C2-C3
76	3I	201	3PH	O11-C1-C2-C3
77	V	605	PTY	O14-C5-C6-C1
79	1G	301	PC7	O3P-C1-C2-C3
81	T	502	PGT	C35-C36-C37-C38
77	1F	403	PTY	N1-C2-C3-O11
75	1B	408	CDL	OB7-CB5-OB6-CB4
75	1B	405	CDL	C77-C78-C79-C80
76	1R	201	3PH	C2F-C2G-C2H-C2I
75	1E	401	CDL	C51-C52-C53-C54
75	1K	101	CDL	C12-C13-C14-C15
76	w	201	3PH	C3A-C3B-C3C-C3D
77	e	302	PTY	C18-C19-C20-C21
76	y	201	3PH	C22-C21-O21-C2
75	W	701	CDL	C36-C37-C38-C39
76	1B	406	3PH	C2E-C2F-C2G-C2H
81	T	502	PGT	C41-C42-C43-C44
77	2F	101	PTY	C2-C3-O11-P1
77	S	302	PTY	C2-C3-O11-P1
77	V	606	PTY	C2-C3-O11-P1
79	1G	301	PC7	C5-C4-O4P-P
75	W	701	CDL	C31-C32-C33-C34
76	1B	406	3PH	C2D-C2E-C2F-C2G
81	l	701	PGT	C38-C39-C40-C41
75	1L	101	CDL	C73-C74-C75-C76
75	x	101	CDL	C58-C59-C60-C61
81	3A	601	PGT	C31-C32-C33-C34
81	b	601	PGT	O4P-C4-C5-C6
75	1K	101	CDL	C80-C81-C82-C83
76	S	301	3PH	C22-C23-C24-C25
75	1B	405	CDL	OA5-CA3-CA4-OA6
75	1K	101	CDL	OA5-CA3-CA4-OA6
75	V	603	CDL	OB5-CB3-CB4-OB6
75	u	602	CDL	OB5-CB3-CB4-OB6
75	u	603	CDL	OB5-CB3-CB4-OB6
75	x	101	CDL	CA7-C31-C32-C33
75	y	202	CDL	OB5-CB3-CB4-OB6
76	1A	406	3PH	O11-C1-C2-O21

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Mol	Chain	Res	Type	Atoms
76	1B	406	3PH	C31-C32-C33-C34
76	1R	201	3PH	O11-C1-C2-O21
76	2D	302	3PH	O11-C1-C2-O21
76	V	601	3PH	O11-C1-C2-O21
81	T	502	PGT	O3P-C1-C2-O2
87	B	501	FMN	N10-C1'-C2'-O2'
79	R	403	PC7	C12-C13-C14-C15
81	b	601	PGT	C40-C41-C42-C43
75	x	101	CDL	C78-C79-C80-C81
76	1B	407	3PH	C39-C3A-C3B-C3C
77	V	606	PTY	C32-C33-C34-C35
75	W	701	CDL	O1-C1-CA2-OA2
79	2A	606	PC7	C4-C5-N-C6
75	x	101	CDL	C82-C83-C84-C85
75	1A	405	CDL	CB3-CB4-CB6-OB8
77	R	406	PTY	O4-C1-C6-C5
77	V	605	PTY	O4-C1-C6-C5
79	1G	301	PC7	O4P-C4-C5-N
75	1A	405	CDL	OB6-CB4-CB6-OB8
75	1B	405	CDL	OB6-CB4-CB6-OB8
75	1E	401	CDL	OA6-CA4-CA6-OA8
75	1K	101	CDL	OA6-CA4-CA6-OA8
75	h	203	CDL	OB6-CB4-CB6-OB8
75	u	603	CDL	OA6-CA4-CA6-OA8
77	1F	403	PTY	O4-C1-C6-O7
77	3F	101	PTY	O4-C1-C6-O7
77	S	302	PTY	C15-C16-C17-C18
77	V	604	PTY	C11-C12-C13-C14
75	R	405	CDL	OA9-CA7-OA8-CA6
75	u	602	CDL	C17-C18-C19-C20
75	x	101	CDL	C52-C53-C54-C55
76	y	201	3PH	C38-C39-C3A-C3B
77	h	202	PTY	C36-C37-C38-C39
76	1K	102	3PH	C3A-C3B-C3C-C3D
76	g	101	3PH	C39-C3A-C3B-C3C
77	h	202	PTY	C33-C34-C35-C36
81	b	601	PGT	C38-C39-C40-C41
75	1B	408	CDL	C34-C35-C36-C37
77	V	605	PTY	C34-C35-C36-C37
79	1G	301	PC7	O11-C11-O3-C3
77	e	302	PTY	C33-C34-C35-C36
75	y	202	CDL	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
76	V	601	3PH	C29-C2A-C2B-C2C
77	e	302	PTY	C40-C41-C42-C43
77	V	606	PTY	C15-C16-C17-C18
79	2A	606	PC7	C4-C5-N-C8
75	1K	101	CDL	C77-C78-C79-C80
76	2I	201	3PH	C33-C34-C35-C36
77	S	302	PTY	C17-C18-C19-C20
77	1F	403	PTY	C32-C33-C34-C35
81	b	601	PGT	C32-C31-O2-C2
77	3D	301	PTY	C8-C11-C12-C13
91	s	401	COO	C2X-C3X-O3X-P3X
75	u	603	CDL	C32-C33-C34-C35
77	V	606	PTY	C36-C37-C38-C39
75	x	101	CDL	C17-C18-C19-C20
75	1B	405	CDL	CB6-CB4-OB6-CB5
75	1L	101	CDL	CB6-CB4-OB6-CB5
75	R	405	CDL	CB6-CB4-OB6-CB5
75	u	602	CDL	CB6-CB4-OB6-CB5
76	V	602	3PH	C1-C2-O21-C21
77	R	404	PTY	C1-C6-O7-C8
77	T	501	PTY	C1-C6-O7-C8
75	1K	101	CDL	OB5-CB3-CB4-CB6
81	l	701	PGT	C21-C22-C23-C24
76	y	201	3PH	O22-C21-O21-C2
82	2A	603	HEA	C11-C12-C13-C14
76	1E	402	3PH	C23-C24-C25-C26
75	1B	405	CDL	C1-CA2-OA2-PA1
89	r	200	8Q1	C28-O27-P24-O3
79	u	601	PC7	C38-C39-C40-C41
76	3D	302	3PH	O11-C1-C2-O21
81	T	505	PGT	O3P-C1-C2-O2
79	2A	606	PC7	C4-C5-N-C7
73	1A	402	UQ5	C12-C11-C9-C8
81	b	601	PGT	O31-C31-O2-C2
76	2I	201	3PH	C31-C32-C33-C34
75	1B	408	CDL	C31-C32-C33-C34
75	W	701	CDL	C84-C85-C86-C87
76	3I	201	3PH	C2A-C2B-C2C-C2D
76	h	201	3PH	C3A-C3B-C3C-C3D
82	2A	602	HEA	C2A-CAA-CBA-CGA
75	1B	408	CDL	C51-CB5-OB6-CB4
75	x	101	CDL	OA6-CA4-CA6-OA8

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Mol	Chain	Res	Type	Atoms
81	2A	601	PGT	O2-C2-C3-O3
76	3D	302	3PH	C27-C28-C29-C2A
77	V	604	PTY	C32-C33-C34-C35
75	1B	405	CDL	CA2-OA2-PA1-OA5
75	1B	408	CDL	CB2-OB2-PB2-OB5
75	1E	401	CDL	CA3-OA5-PA1-OA2
75	u	602	CDL	CB3-OB5-PB2-OB2
75	y	202	CDL	CB3-OB5-PB2-OB2
77	2D	301	PTY	C3-O11-P1-O14
77	G	303	PTY	C3-O11-P1-O14
77	R	406	PTY	C3-O11-P1-O14
77	T	504	PTY	C3-O11-P1-O14
77	V	606	PTY	C3-O11-P1-O14
77	e	302	PTY	C3-O11-P1-O14
77	x	102	PTY	C3-O11-P1-O14
79	1G	301	PC7	C1-O3P-P-O4P
79	Q	302	PC7	C1-O3P-P-O4P
79	T	503	PC7	C4-O4P-P-O3P
81	3A	601	PGT	C1-O3P-P-O4P
81	b	601	PGT	C4-O4P-P-O3P
75	1A	405	CDL	C36-C37-C38-C39
75	R	405	CDL	C52-C53-C54-C55
76	V	601	3PH	C2D-C2E-C2F-C2G
75	W	701	CDL	CB3-CB4-CB6-OB8
79	R	403	PC7	C1-C2-C3-O3
76	1B	406	3PH	C25-C26-C27-C28
76	V	601	3PH	C23-C24-C25-C26
76	1B	407	3PH	C2C-C2D-C2E-C2F
90	P	401	NDP	O4D-C1D-N1N-C6N
75	x	101	CDL	CA5-C11-C12-C13
76	V	601	3PH	C33-C34-C35-C36
91	s	401	COO	P1A-O3A-P2A-O5A
77	2D	301	PTY	C13-C14-C15-C16
77	R	406	PTY	C35-C36-C37-C38
76	2I	201	3PH	C32-C33-C34-C35
77	1E	403	PTY	C35-C36-C37-C38
75	1B	405	CDL	C80-C81-C82-C83
75	u	603	CDL	C17-C18-C19-C20
89	J	200	8Q1	C11-C12-C13-C14
75	u	602	CDL	CA4-CA3-OA5-PA1
76	S	301	3PH	C2-C1-O11-P
79	1G	301	PC7	C2-C1-O3P-P

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Mol	Chain	Res	Type	Atoms
75	1B	405	CDL	CA2-C1-CB2-OB2
75	1E	401	CDL	CB2-C1-CA2-OA2
75	1L	101	CDL	CB2-C1-CA2-OA2
75	x	101	CDL	C14-C15-C16-C17
76	V	602	3PH	C33-C34-C35-C36
81	l	701	PGT	C37-C38-C39-C40
75	u	602	CDL	CA7-C31-C32-C33
90	P	401	NDP	C2D-C1D-N1N-C6N
77	G	303	PTY	C33-C34-C35-C36
77	x	102	PTY	C31-C32-C33-C34
75	1M	501	CDL	C36-C37-C38-C39
77	R	404	PTY	C22-C23-C24-C25
79	1H	101	PC7	C4-C5-N-C7
77	x	102	PTY	C40-C41-C42-C43
75	1L	101	CDL	OB5-CB3-CB4-OB6
75	W	701	CDL	C42-C43-C44-C45
76	1A	406	3PH	C28-C29-C2A-C2B
77	h	202	PTY	C8-C11-C12-C13
76	V	601	3PH	C34-C35-C36-C37
76	3I	201	3PH	C22-C23-C24-C25
77	V	605	PTY	C17-C18-C19-C20
91	s	401	COO	O2-C1-C13-C11
76	R	401	3PH	C37-C38-C39-C3A
81	2A	601	PGT	O31-C31-O2-C2
77	x	102	PTY	C38-C39-C40-C41
75	y	202	CDL	C32-C33-C34-C35
75	1E	401	CDL	C72-C73-C74-C75
77	h	202	PTY	C41-C42-C43-C44
77	e	301	PTY	O4-C1-C6-O7
79	1G	301	PC7	O2-C2-C3-O3
75	R	405	CDL	C1-CB2-OB2-PB2
77	3D	301	PTY	C6-C5-O14-P1
77	V	605	PTY	C12-C11-C8-O10
77	1F	403	PTY	C35-C36-C37-C38
77	e	302	PTY	C14-C15-C16-C17
75	1L	101	CDL	C13-C14-C15-C16
75	1K	101	CDL	C79-C80-C81-C82
75	x	101	CDL	C71-C72-C73-C74
75	1L	101	CDL	C31-C32-C33-C34
76	2D	302	3PH	C35-C36-C37-C38
90	P	401	NDP	C3D-C4D-C5D-O5D
77	R	402	PTY	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
76	V	602	3PH	C1-C2-C3-O31
76	w	201	3PH	C1-C2-C3-O31
77	x	102	PTY	O4-C1-C6-C5
75	V	603	CDL	C17-C18-C19-C20
79	u	601	PC7	C35-C36-C37-C38
77	V	606	PTY	C16-C17-C18-C19
77	h	202	PTY	C38-C39-C40-C41
75	W	701	CDL	CA7-C31-C32-C33
75	1B	408	CDL	C15-C16-C17-C18
81	b	601	PGT	C34-C35-C36-C37
91	s	401	COO	N1-C1-C13-C11
79	3A	606	PC7	C1-C2-O2-C31
77	3D	301	PTY	C18-C19-C20-C21
79	1H	101	PC7	C4-C5-N-C8
75	h	203	CDL	C72-C71-CB7-OB8
74	1A	404	HEM	CAD-CBD-CGD-O1D
76	y	201	3PH	C32-C33-C34-C35
75	1B	408	CDL	CB3-OB5-PB2-OB2
77	R	406	PTY	C32-C33-C34-C35
75	1B	405	CDL	C1-CB2-OB2-PB2
75	1E	401	CDL	CB4-CB3-OB5-PB2
81	l	701	PGT	O5-C5-C6-O6
75	1B	408	CDL	C56-C57-C58-C59
76	1A	406	3PH	C26-C27-C28-C29
75	y	202	CDL	CA5-C11-C12-C13
81	2A	601	PGT	O3P-C1-C2-O2
75	1B	405	CDL	C71-C72-C73-C74
76	1B	407	3PH	C28-C29-C2A-C2B
89	J	200	8Q1	C13-C14-C15-C16
76	w	201	3PH	C22-C23-C24-C25
81	2A	601	PGT	C32-C31-O2-C2
76	2I	201	3PH	C34-C35-C36-C37
73	1B	402	UQ5	C12-C11-C9-C10
79	u	601	PC7	C37-C38-C39-C40
74	1B	404	HEM	CAA-CBA-CGA-O1A
76	1K	102	3PH	O21-C2-C3-O31
75	h	203	CDL	C13-C14-C15-C16
76	1B	407	3PH	C27-C28-C29-C2A
77	1E	403	PTY	C11-C12-C13-C14
79	R	403	PC7	C36-C37-C38-C39
75	h	203	CDL	C54-C55-C56-C57
76	c	101	3PH	C34-C35-C36-C37

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Mol	Chain	Res	Type	Atoms
73	Q	301	UQ5	C14-C16-C17-C18
74	1B	404	HEM	CAA-CBA-CGA-O2A
77	T	506	PTY	C14-C15-C16-C17
75	u	602	CDL	C72-C71-CB7-OB8
89	r	200	8Q1	C6-C7-C8-C9
77	V	606	PTY	C31-C32-C33-C34
75	1B	408	CDL	C54-C55-C56-C57
75	W	701	CDL	C55-C56-C57-C58
75	1E	401	CDL	CA3-CA4-CA6-OA8
77	V	606	PTY	O4-C1-C6-C5
75	1B	408	CDL	CB7-C71-C72-C73
75	1K	101	CDL	CA5-C11-C12-C13
82	2A	602	HEA	CAA-CBA-CGA-O2A
77	T	504	PTY	C33-C34-C35-C36
89	J	200	8Q1	O4-C1-S44-C43
76	g	101	3PH	C24-C25-C26-C27
74	1A	404	HEM	CAA-CBA-CGA-O2A
76	V	602	3PH	C3A-C3B-C3C-C3D
75	h	203	CDL	OA5-CA3-CA4-OA6
77	V	605	PTY	O14-C5-C6-O7
76	V	602	3PH	C23-C24-C25-C26
74	1A	404	HEM	CAA-CBA-CGA-O1A
75	u	603	CDL	C43-C44-C45-C46
76	w	201	3PH	C35-C36-C37-C38
75	R	405	CDL	C33-C34-C35-C36
81	2A	601	PGT	C15-C16-C17-C18
77	2F	101	PTY	O14-C5-C6-C1
77	T	504	PTY	O14-C5-C6-C1
82	2A	602	HEA	C26-C15-C16-C17
73	1A	402	UQ5	C18-C19-C21-C22
74	1B	403	HEM	CAD-CBD-CGD-O2D
75	x	101	CDL	C35-C36-C37-C38
81	3A	601	PGT	O5-C5-C6-O6
81	l	701	PGT	C33-C34-C35-C36
77	h	202	PTY	O4-C1-C6-O7
76	1B	406	3PH	C2C-C2D-C2E-C2F
74	1B	403	HEM	CAD-CBD-CGD-O1D
76	1E	402	3PH	O21-C21-C22-C23
77	2D	301	PTY	C12-C11-C8-O7
76	1R	201	3PH	C1-O11-P-O13
76	2D	302	3PH	C24-C25-C26-C27
91	s	401	COO	C3X-O3X-P3X-O9A

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Mol	Chain	Res	Type	Atoms
77	e	302	PTY	C12-C11-C8-O7
76	w	201	3PH	C34-C35-C36-C37
82	3A	602	HEA	C26-C15-C16-C17
73	1B	402	UQ5	C12-C11-C9-C8
79	R	403	PC7	C44-C45-C46-C47
77	1F	403	PTY	O4-C30-C31-C32
79	3A	606	PC7	O2-C31-C32-C33
75	1B	408	CDL	C14-C15-C16-C17
76	h	201	3PH	C24-C25-C26-C27
76	w	201	3PH	C2B-C2C-C2D-C2E
75	1K	101	CDL	C53-C54-C55-C56
75	x	101	CDL	C33-C34-C35-C36
75	1F	401	CDL	O1-C1-CA2-OA2
75	u	603	CDL	C12-C11-CA5-OA6
79	3A	606	PC7	O3-C11-C12-C13
75	1E	401	CDL	CB3-CB4-OB6-CB5
75	1E	401	CDL	CB6-CB4-OB6-CB5
75	1B	408	CDL	CA5-C11-C12-C13
73	Q	301	UQ5	C11-C12-C13-C14
89	J	200	8Q1	C9-C10-C11-C12
77	T	506	PTY	O10-C8-O7-C6
79	T	503	PC7	C37-C38-C39-C40
74	1A	403	HEM	CAD-CBD-CGD-O2D
82	2A	602	HEA	CAD-CBD-CGD-O2D
76	S	301	3PH	C27-C28-C29-C2A
75	x	101	CDL	C52-C51-CB5-OB6
75	x	101	CDL	C72-C71-CB7-OB8
76	1K	102	3PH	O21-C21-C22-C23
76	w	201	3PH	C32-C33-C34-C35
77	1F	403	PTY	C17-C18-C19-C20
77	S	302	PTY	C12-C11-C8-O7
77	2F	101	PTY	C11-C12-C13-C14
73	Q	301	UQ5	C5-C4-O4-C4M
76	R	401	3PH	C1-O11-P-O12
76	V	601	3PH	C1-O11-P-O12
77	2F	101	PTY	O4-C1-C6-C5
81	l	701	PGT	C1-C2-C3-O3
82	2A	602	HEA	CAA-CBA-CGA-O1A
79	3A	606	PC7	O3P-C1-C2-O2
74	1A	404	HEM	CAD-CBD-CGD-O2D
82	2A	602	HEA	CAD-CBD-CGD-O1D
82	3A	602	HEA	CAD-CBD-CGD-O1D

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Mol	Chain	Res	Type	Atoms
82	3A	602	HEA	CAD-CBD-CGD-O2D
77	R	406	PTY	C16-C17-C18-C19
77	h	202	PTY	O4-C30-C31-C32
76	V	601	3PH	C2A-C2B-C2C-C2D
81	l	701	PGT	C35-C36-C37-C38
74	1A	403	HEM	CAD-CBD-CGD-O1D
75	1E	401	CDL	C72-C71-CB7-OB8
75	x	101	CDL	C76-C77-C78-C79
77	2D	301	PTY	C15-C16-C17-C18
75	1L	101	CDL	OB5-CB3-CB4-CB6
75	u	603	CDL	OB5-CB3-CB4-CB6
77	1E	403	PTY	O14-C5-C6-C1
81	2A	601	PGT	O3P-C1-C2-C3
75	1K	101	CDL	C52-C51-CB5-OB6
75	R	405	CDL	C72-C71-CB7-OB8
76	2D	302	3PH	O21-C21-C22-C23
79	1G	301	PC7	O3-C11-C12-C13
79	3A	606	PC7	C4-C5-N-C7
91	s	401	COO	C3X-O3X-P3X-O8A
76	w	201	3PH	C39-C3A-C3B-C3C
75	1K	101	CDL	C12-C11-CA5-OA6
73	1A	401	UQ5	C12-C11-C9-C10
77	R	404	PTY	C17-C18-C19-C20
81	T	502	PGT	C31-C32-C33-C34
77	h	202	PTY	C14-C15-C16-C17
77	x	102	PTY	C21-C22-C23-C24
75	u	603	CDL	C52-C51-CB5-OB6
75	x	101	CDL	C81-C82-C83-C84
77	e	302	PTY	C12-C11-C8-O10
76	V	601	3PH	C27-C28-C29-C2A
75	1B	405	CDL	C12-C11-CA5-OA6
77	2D	301	PTY	C12-C11-C8-O10
81	T	502	PGT	O31-C31-C32-C33
77	T	506	PTY	C11-C8-O7-C6
82	3A	602	HEA	CAA-CBA-CGA-O2A
77	S	302	PTY	C12-C11-C8-O10
76	3I	201	3PH	C38-C39-C3A-C3B
76	g	101	3PH	C23-C24-C25-C26
75	1F	401	CDL	C72-C71-CB7-OB8
75	u	602	CDL	C32-C33-C34-C35
79	3A	606	PC7	C4-C5-N-C6
76	3I	201	3PH	C35-C36-C37-C38

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Mol	Chain	Res	Type	Atoms
76	1E	402	3PH	O22-C21-C22-C23
79	3A	606	PC7	O31-C31-C32-C33
75	V	603	CDL	CA2-C1-CB2-OB2
76	V	602	3PH	C35-C36-C37-C38
76	1R	201	3PH	C28-C29-C2A-C2B
76	2D	302	3PH	C25-C26-C27-C28
73	1B	402	UQ5	C11-C12-C13-C14
89	J	200	8Q1	C6-C7-C8-C9
75	x	101	CDL	C52-C51-CB5-OB7
77	h	202	PTY	O30-C30-C31-C32
75	u	603	CDL	CA3-CA4-CA6-OA8
77	e	301	PTY	O4-C1-C6-C5
79	R	403	PC7	C16-C17-C18-C19
75	R	405	CDL	CB3-OB5-PB2-OB2
75	V	603	CDL	CA2-OA2-PA1-OA5
75	x	101	CDL	CB2-OB2-PB2-OB5
81	l	701	PGT	O4P-C4-C5-O5
75	1B	405	CDL	C12-C11-CA5-OA7
77	1F	403	PTY	O30-C30-C31-C32
75	R	405	CDL	C34-C35-C36-C37
75	W	701	CDL	C41-C42-C43-C44
76	V	602	3PH	C32-C33-C34-C35
75	1A	405	CDL	CA4-CA3-OA5-PA1
76	2I	201	3PH	C36-C37-C38-C39
75	1K	101	CDL	C52-C51-CB5-OB7
75	1B	408	CDL	CB3-OB5-PB2-OB3
75	1M	501	CDL	CA3-OA5-PA1-OA3
75	V	603	CDL	CA3-OA5-PA1-OA4
75	u	602	CDL	CB3-OB5-PB2-OB3
75	x	101	CDL	CB2-OB2-PB2-OB4
75	x	101	CDL	CB3-OB5-PB2-OB3
75	y	202	CDL	CB3-OB5-PB2-OB3
77	2D	301	PTY	C3-O11-P1-O13
77	R	406	PTY	C3-O11-P1-O13
81	T	505	PGT	C4-O4P-P-O1P
81	b	601	PGT	C4-O4P-P-O2P
81	l	701	PGT	C4-O4P-P-O2P
75	1E	401	CDL	C72-C71-CB7-OB9
75	u	603	CDL	C52-C51-CB5-OB7
75	x	101	CDL	C72-C71-CB7-OB9
76	1K	102	3PH	O22-C21-C22-C23
75	1K	101	CDL	C32-C31-CA7-OA8

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Mol	Chain	Res	Type	Atoms
82	2A	602	HEA	C19-C20-C21-C22
76	V	602	3PH	C25-C26-C27-C28
76	2D	302	3PH	O22-C21-C22-C23
79	3A	606	PC7	O11-C11-C12-C13
76	c	101	3PH	C37-C38-C39-C3A
77	1F	403	PTY	C15-C16-C17-C18
75	1E	401	CDL	C52-C51-CB5-OB6
76	c	101	3PH	C2D-C2E-C2F-C2G
79	R	403	PC7	C13-C14-C15-C16
75	1B	405	CDL	C82-C83-C84-C85
81	b	601	PGT	C31-C32-C33-C34
76	w	201	3PH	C36-C37-C38-C39
77	1F	403	PTY	C2-C3-O11-P1
77	h	202	PTY	C2-C3-O11-P1
79	3A	606	PC7	C5-C4-O4P-P
82	3A	602	HEA	C3B-C11-C12-C13
75	u	603	CDL	C35-C36-C37-C38
75	1A	405	CDL	C32-C31-CA7-OA8
77	V	606	PTY	C33-C34-C35-C36
82	3A	602	HEA	CAA-CBA-CGA-O1A
79	1G	301	PC7	O11-C11-C12-C13
75	h	203	CDL	C12-C11-CA5-OA6
77	1E	403	PTY	C12-C11-C8-O7
75	1A	405	CDL	C35-C36-C37-C38
76	1B	406	3PH	C2B-C2C-C2D-C2E
74	1B	404	HEM	CAD-CBD-CGD-O1D
75	R	405	CDL	C35-C36-C37-C38
75	h	203	CDL	C52-C51-CB5-OB6
77	V	605	PTY	O4-C30-C31-C32
77	x	102	PTY	C23-C24-C25-C26
77	1E	403	PTY	O14-C5-C6-O7
77	2D	301	PTY	O14-C5-C6-O7
77	2F	101	PTY	O14-C5-C6-O7
75	1F	401	CDL	C72-C71-CB7-OB9
75	1K	101	CDL	C12-C11-CA5-OA7
75	x	101	CDL	C12-C11-CA5-OA7
75	x	101	CDL	C12-C11-CA5-OA6
75	h	203	CDL	C52-C51-CB5-OB7
75	u	603	CDL	O1-C1-CA2-OA2
76	1B	407	3PH	C34-C35-C36-C37
76	V	601	3PH	C2F-C2G-C2H-C2I
75	1K	101	CDL	C32-C31-CA7-OA9

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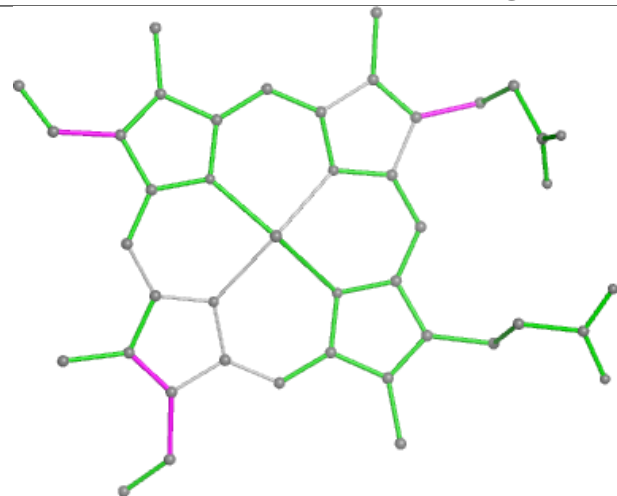
Mol	Chain	Res	Type	Atoms
75	R	405	CDL	C72-C71-CB7-OB9
76	1B	407	3PH	C26-C27-C28-C29
77	h	202	PTY	C37-C38-C39-C40

There are no ring outliers.

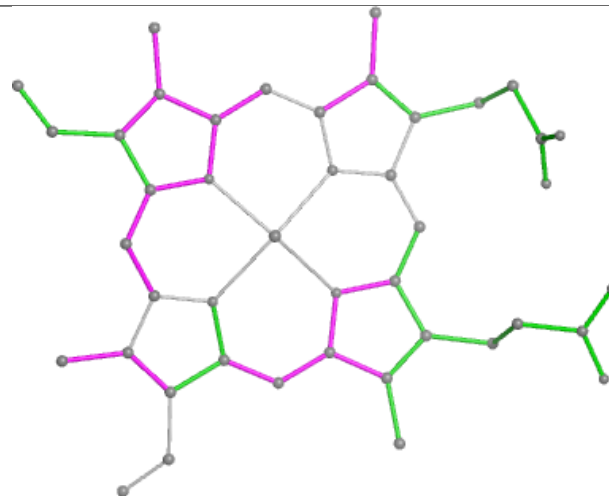
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

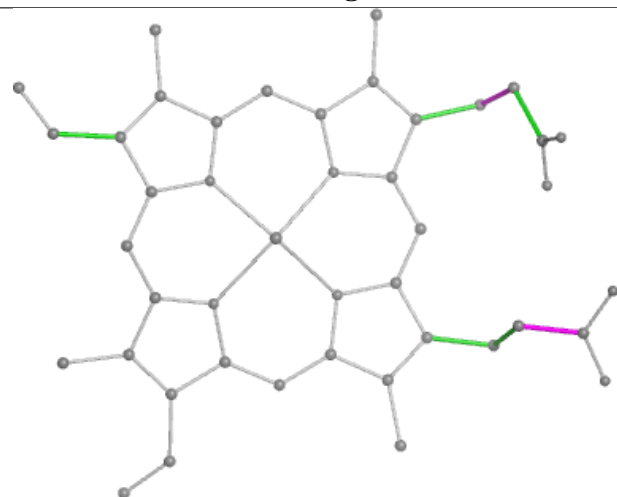
Ligand HEM 1A 403



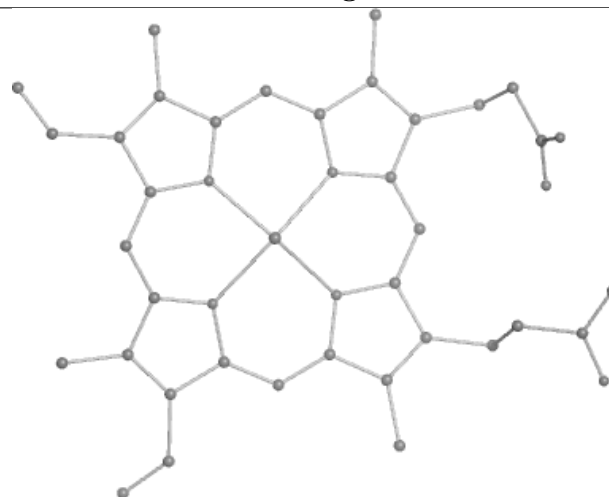
Bond lengths



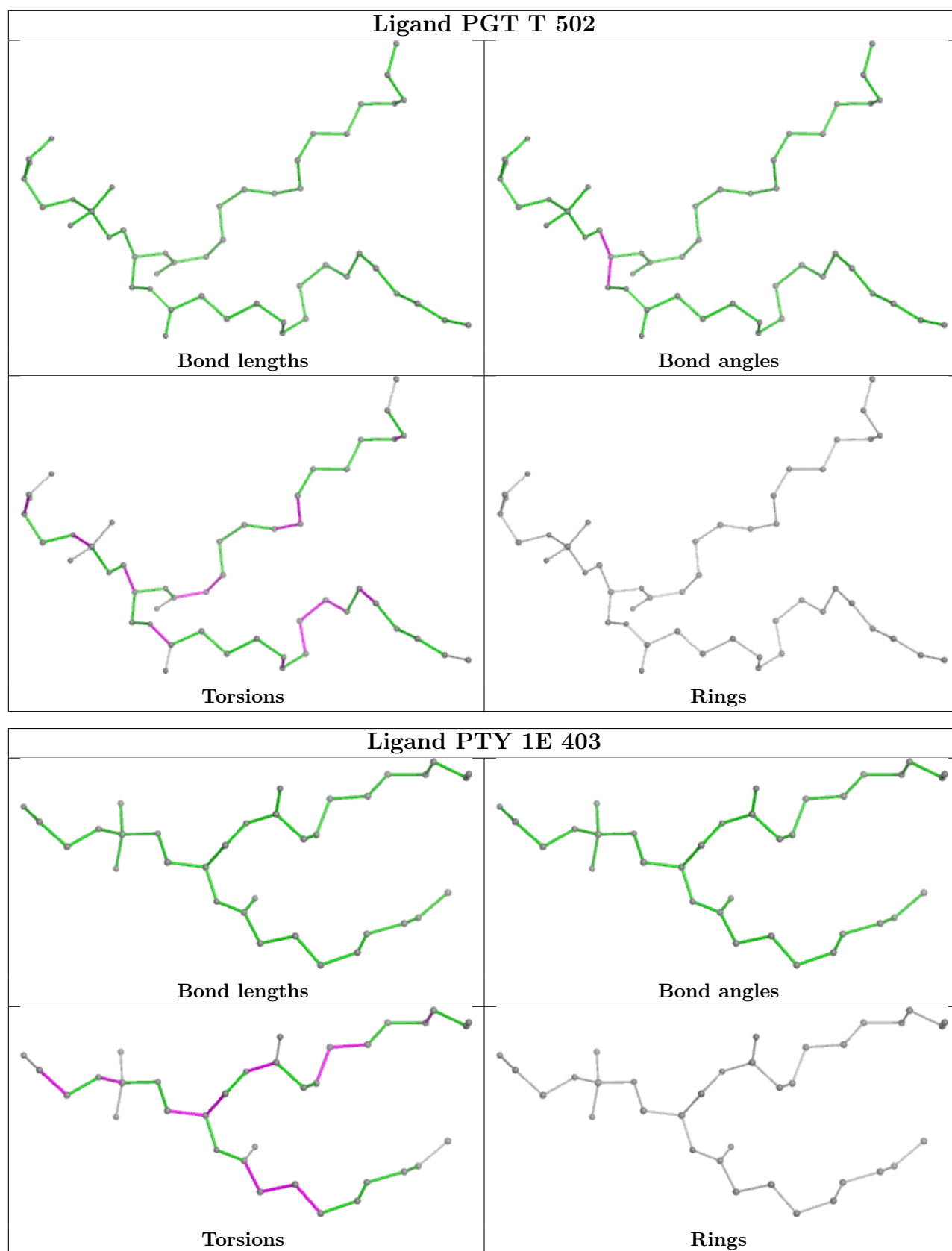
Bond angles

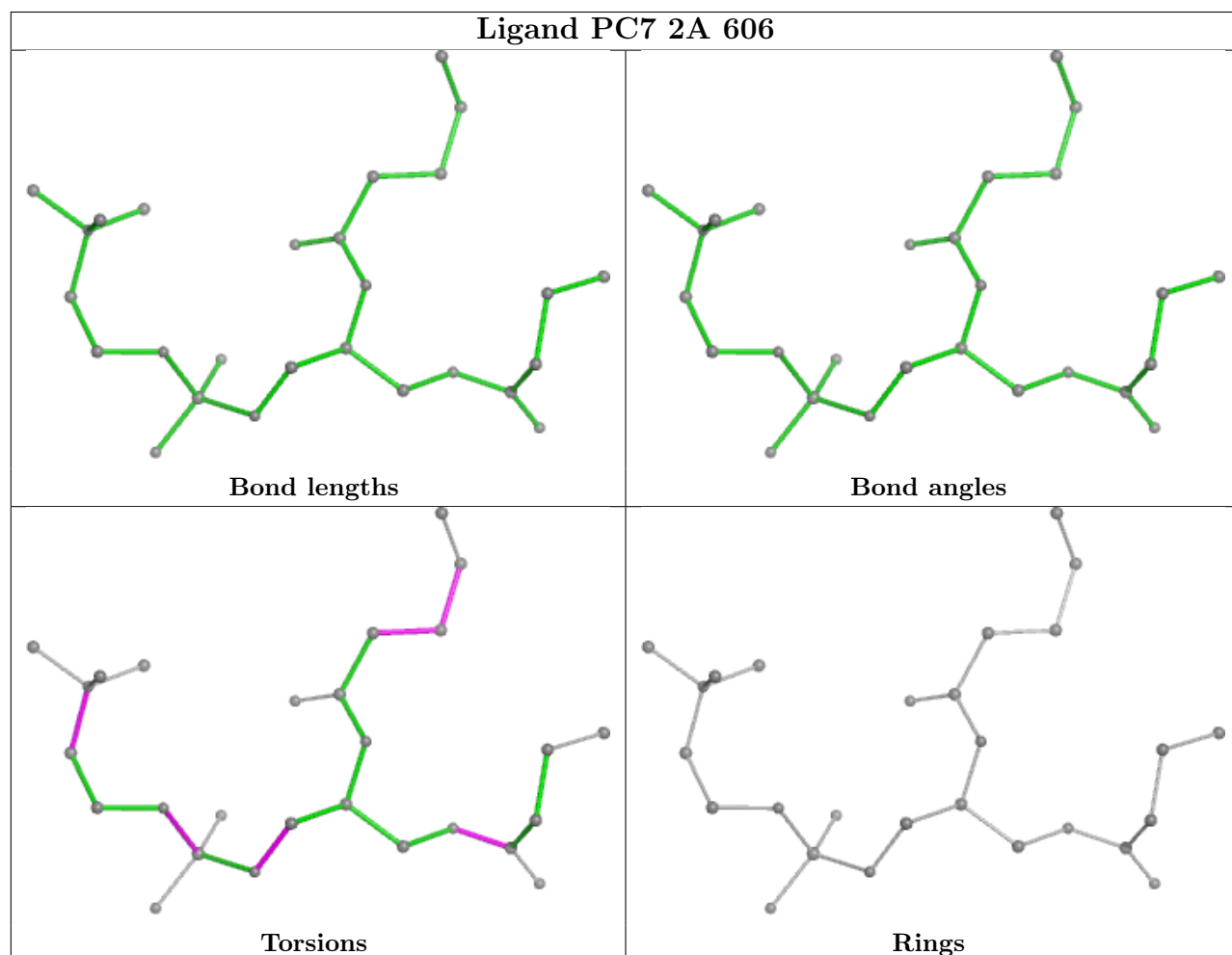
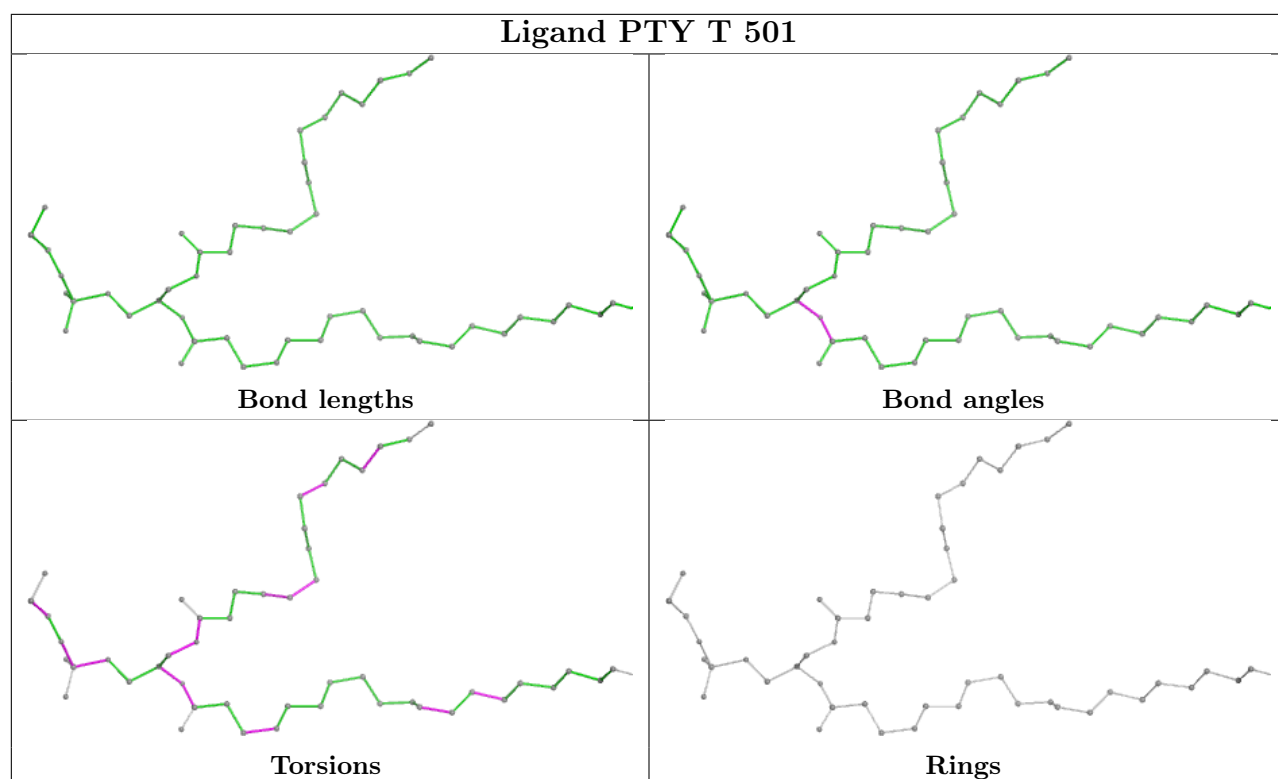


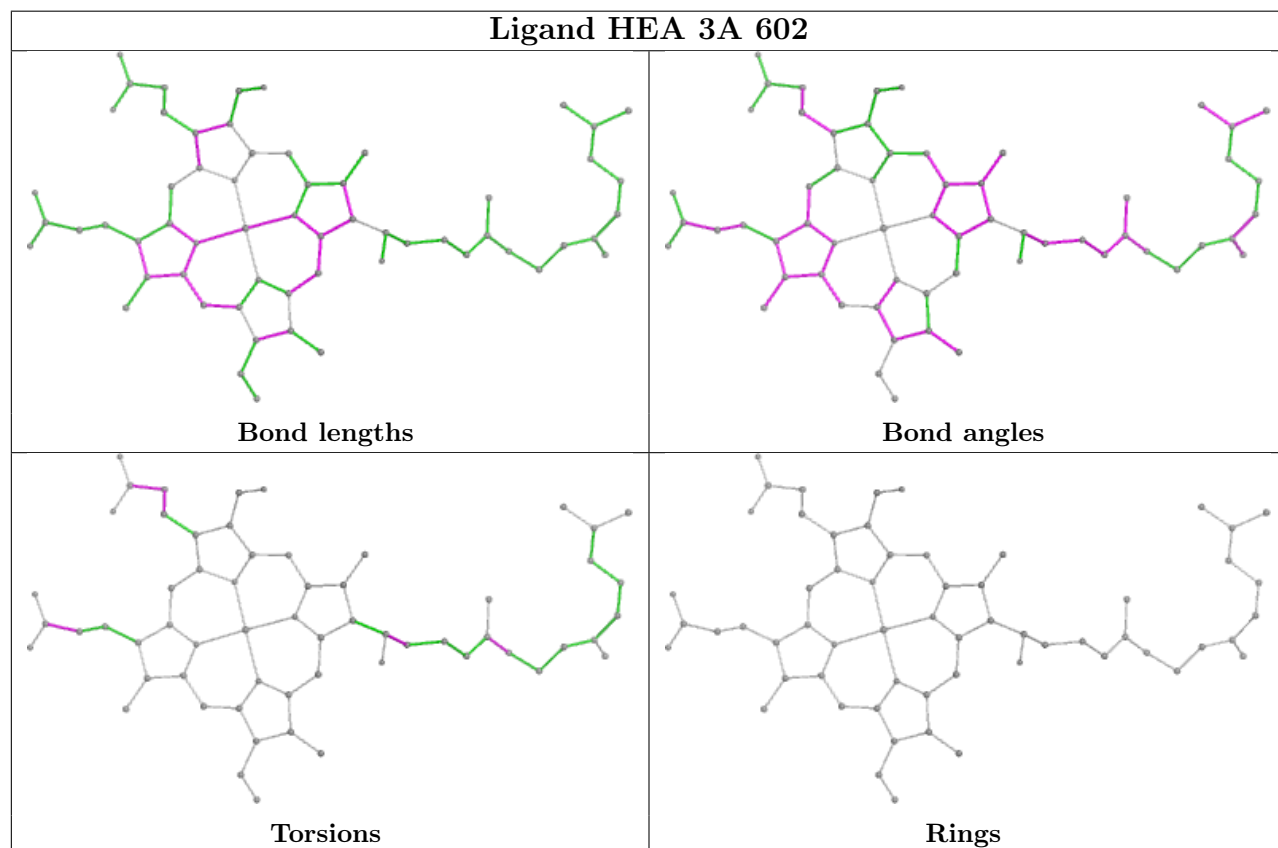
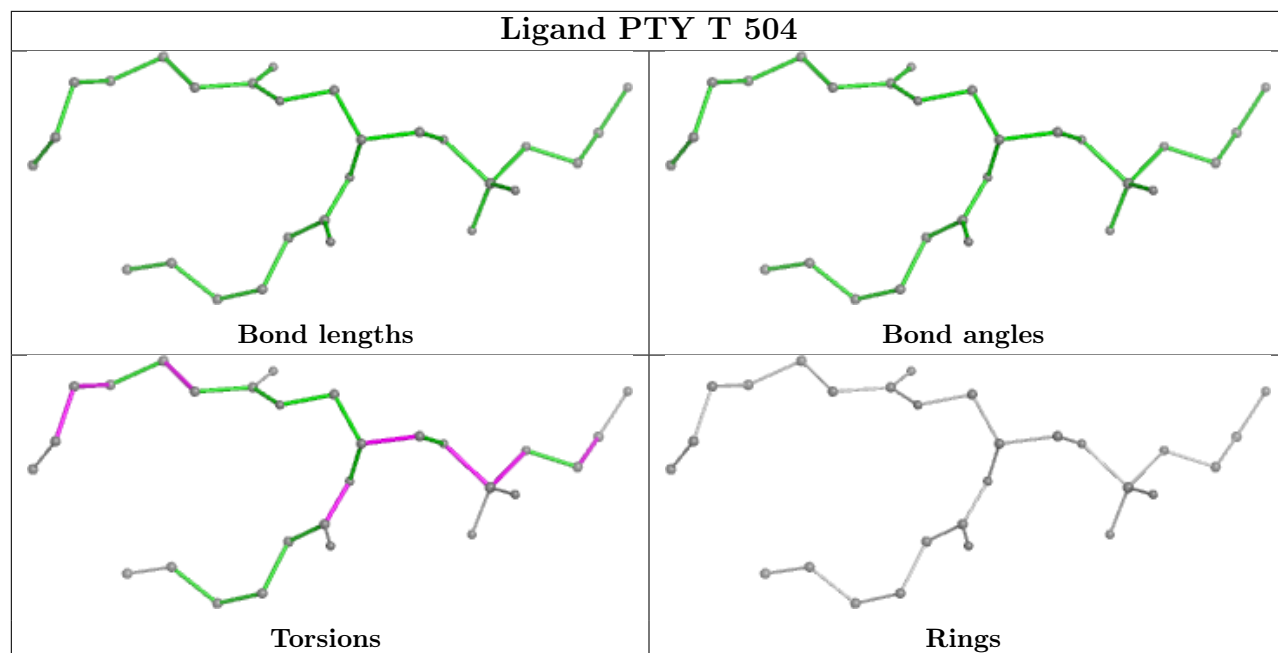
Torsions

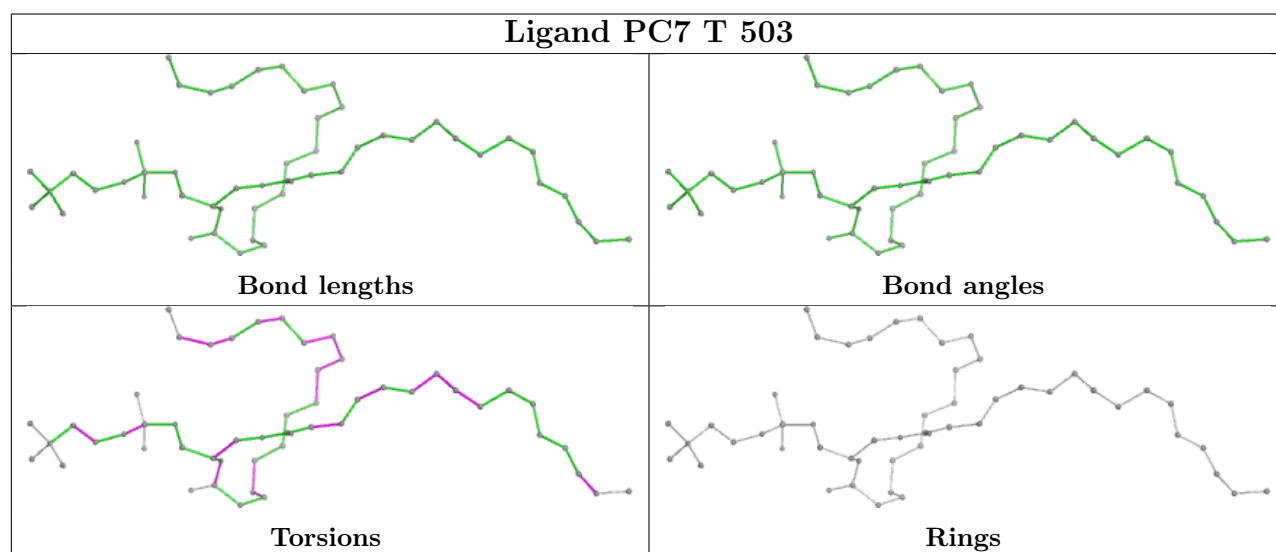
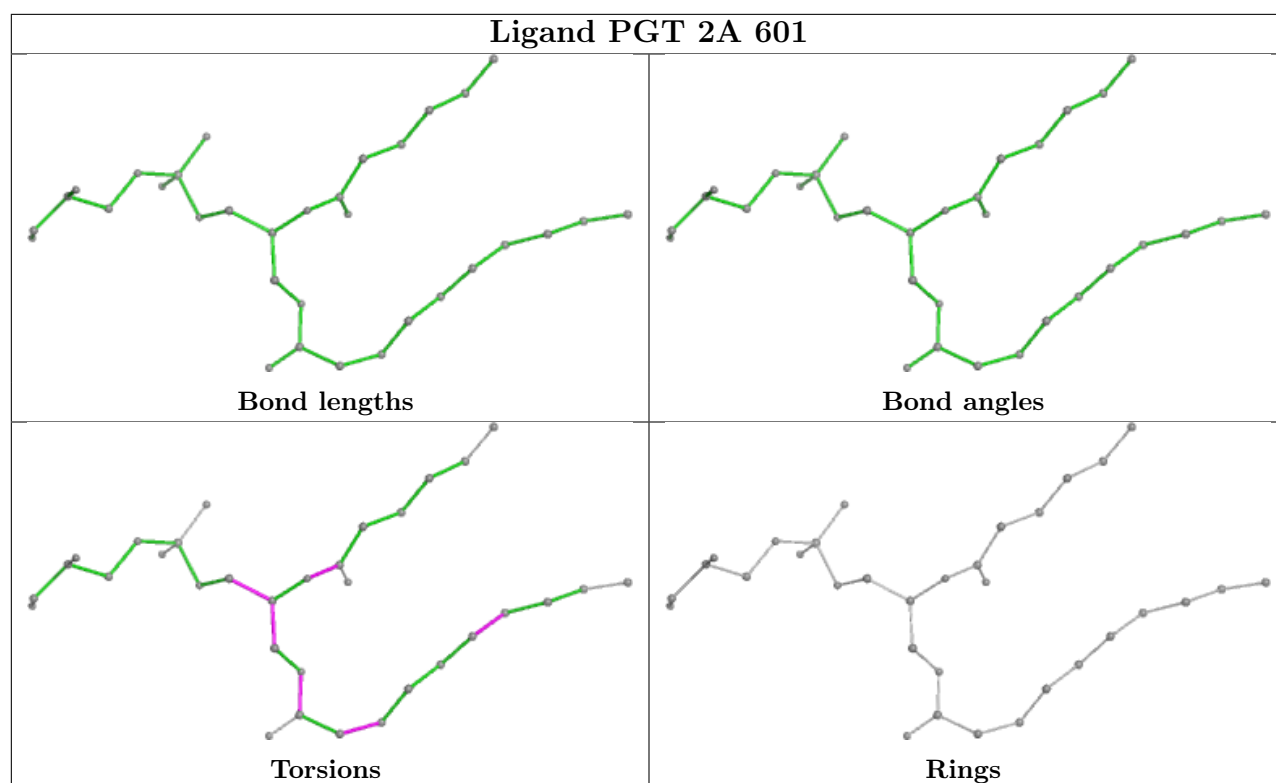


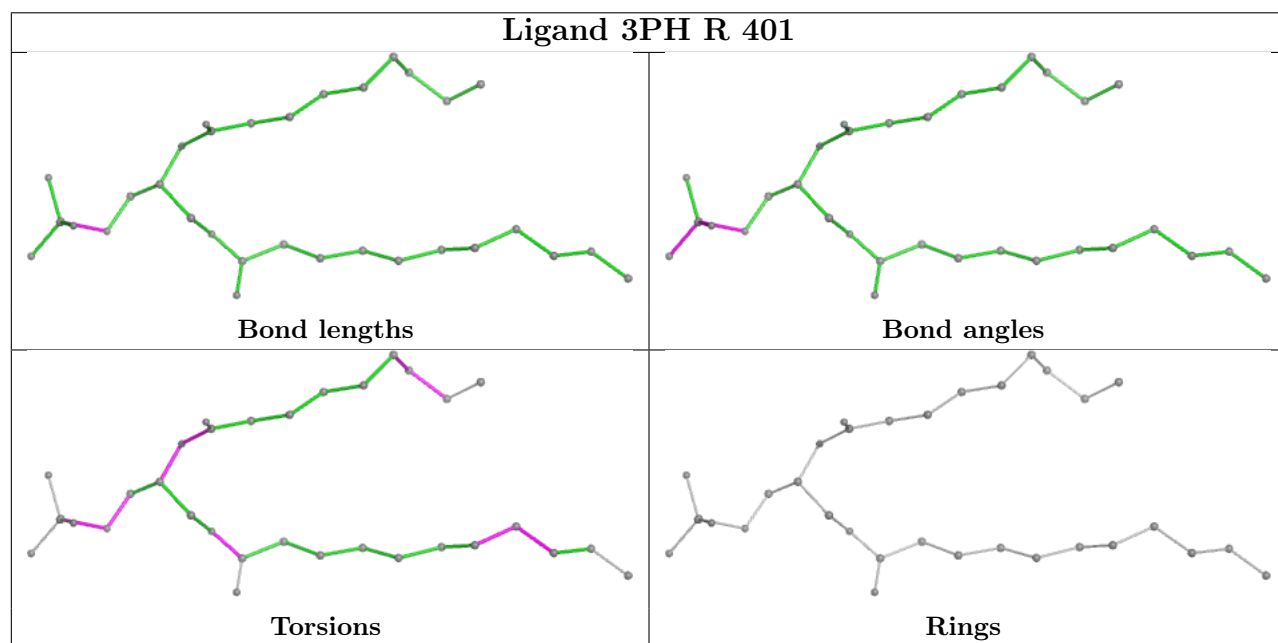
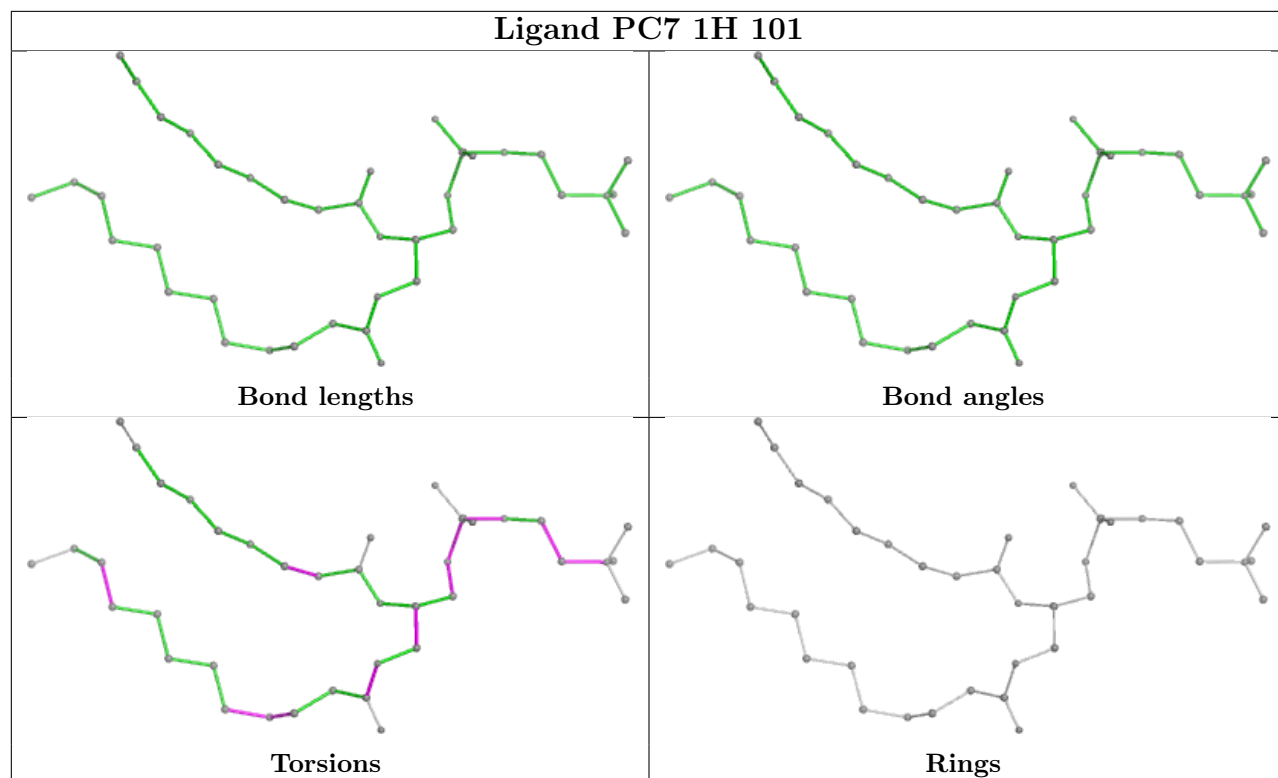
Rings

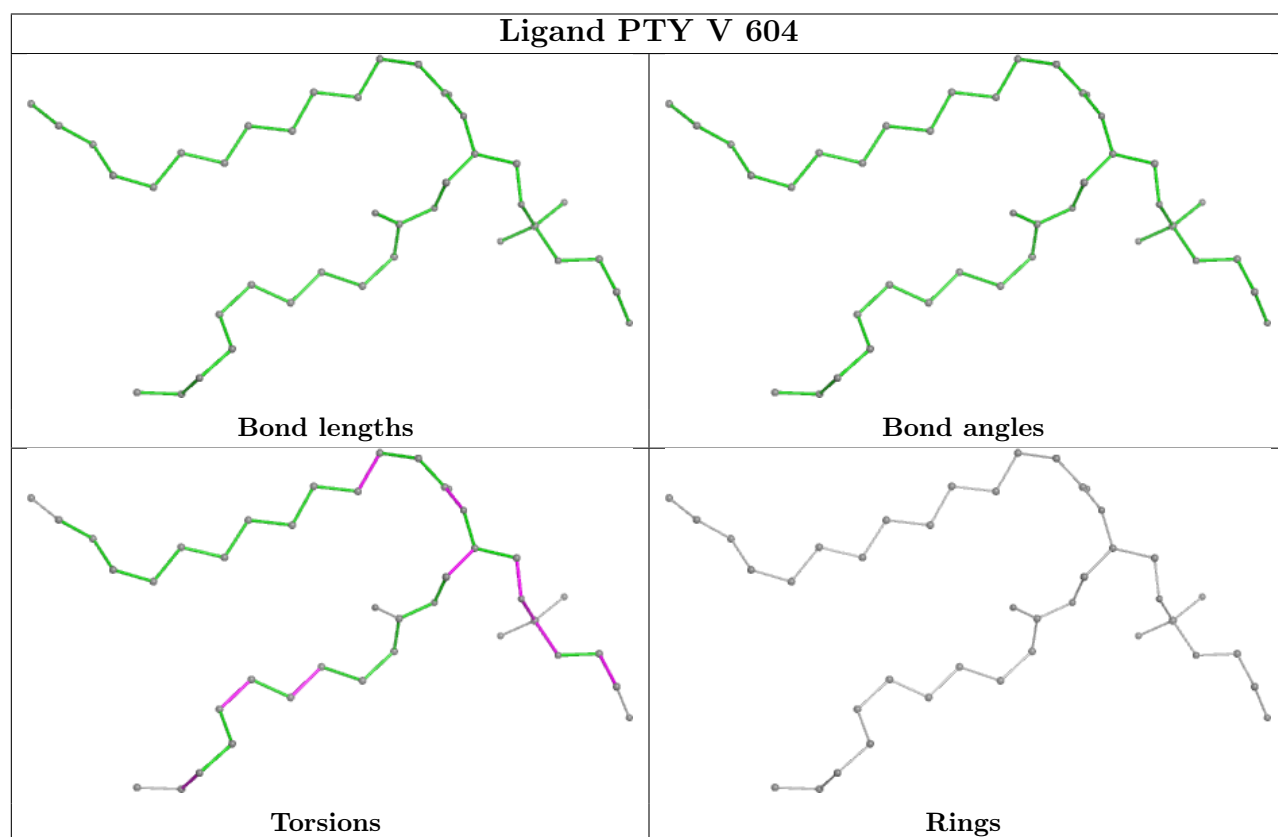
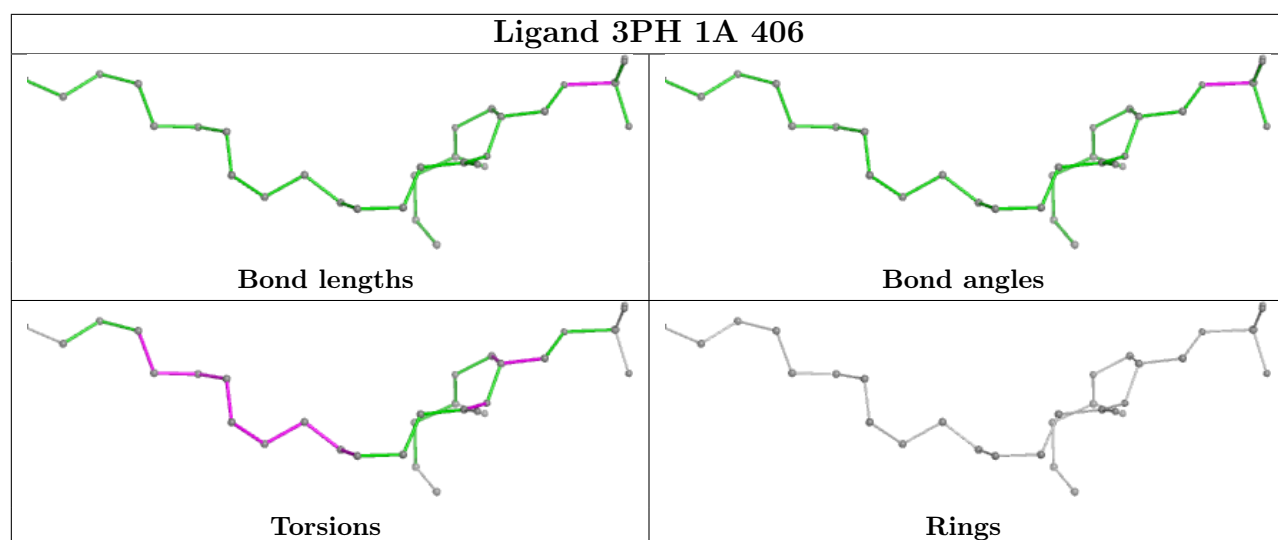


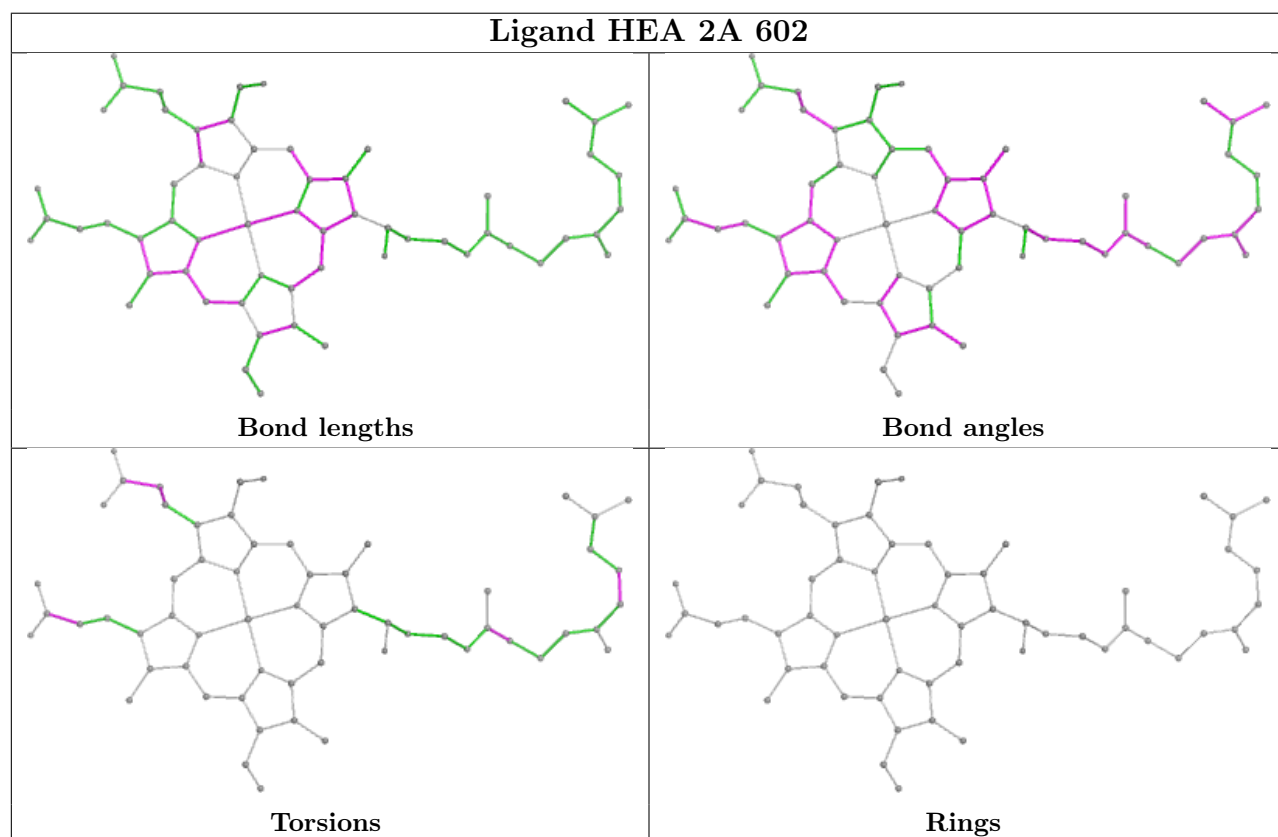
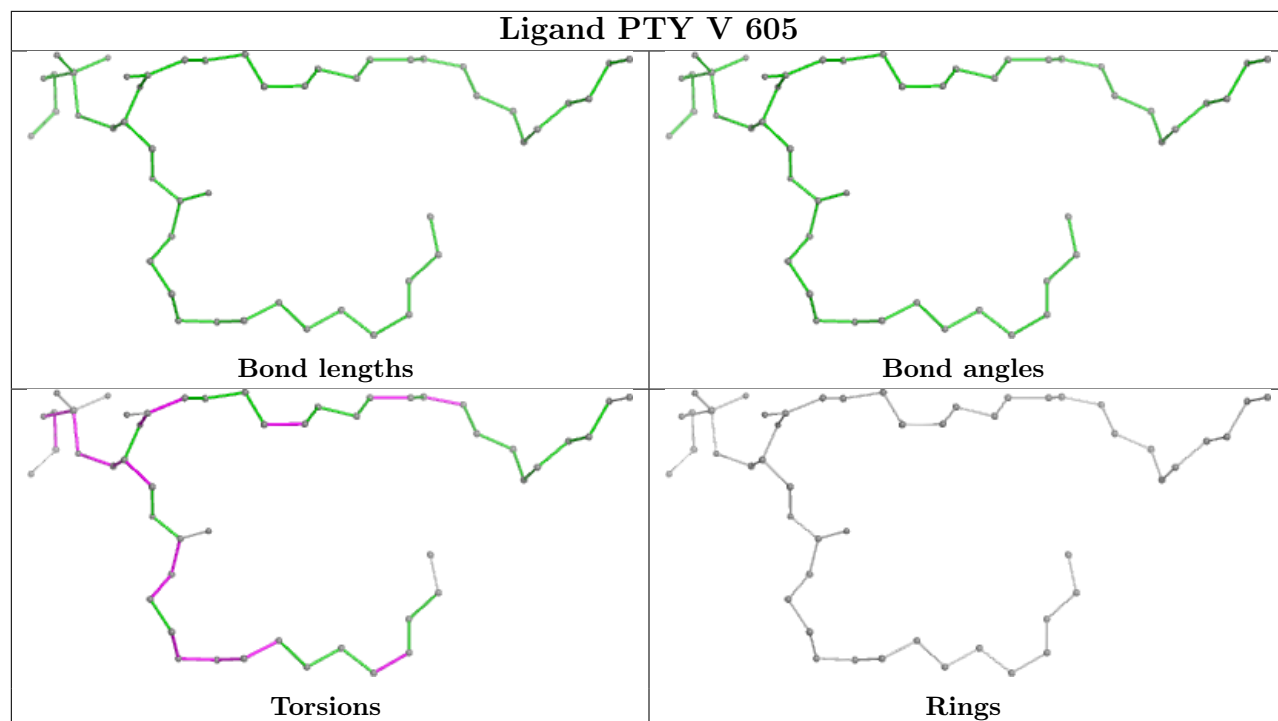


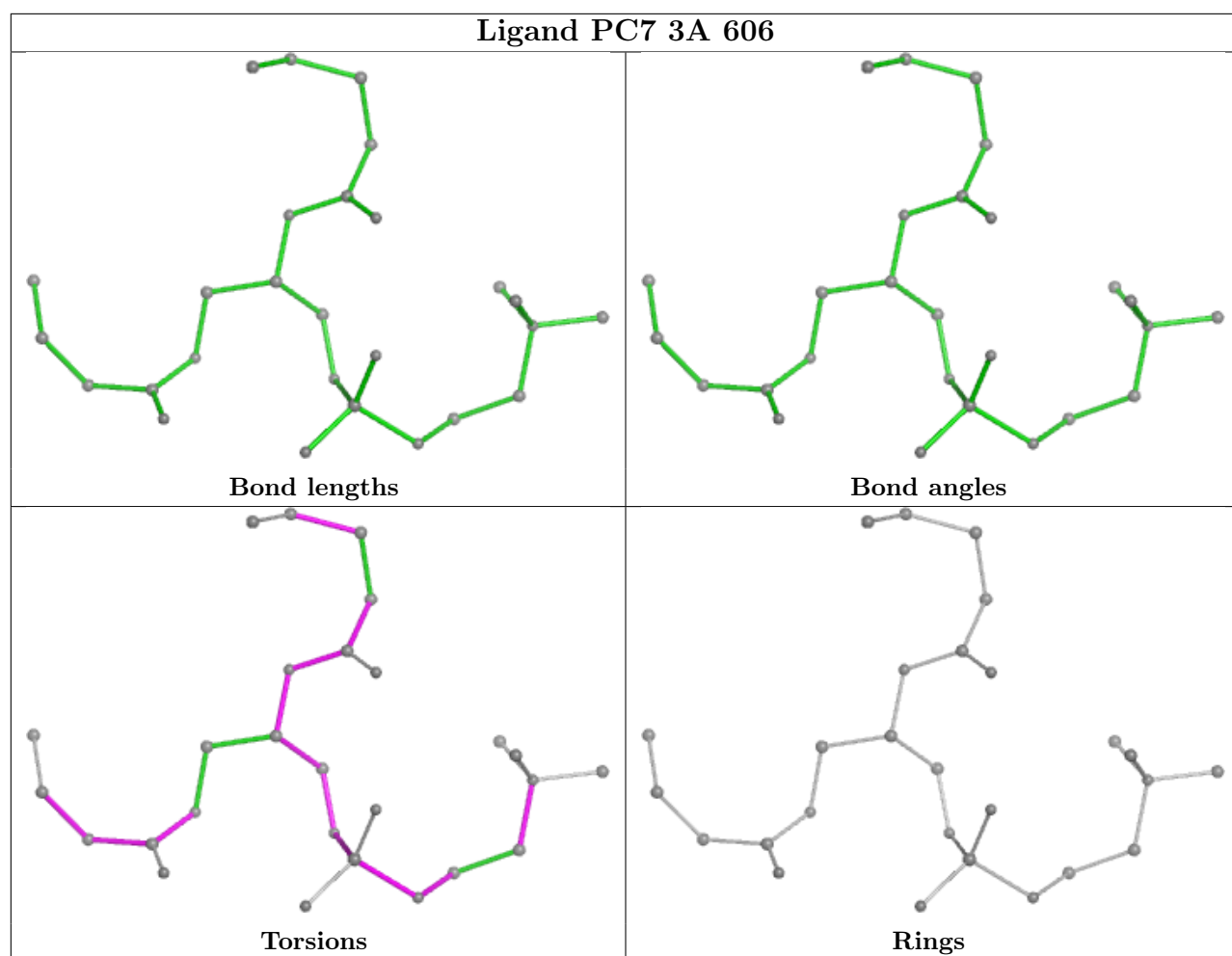


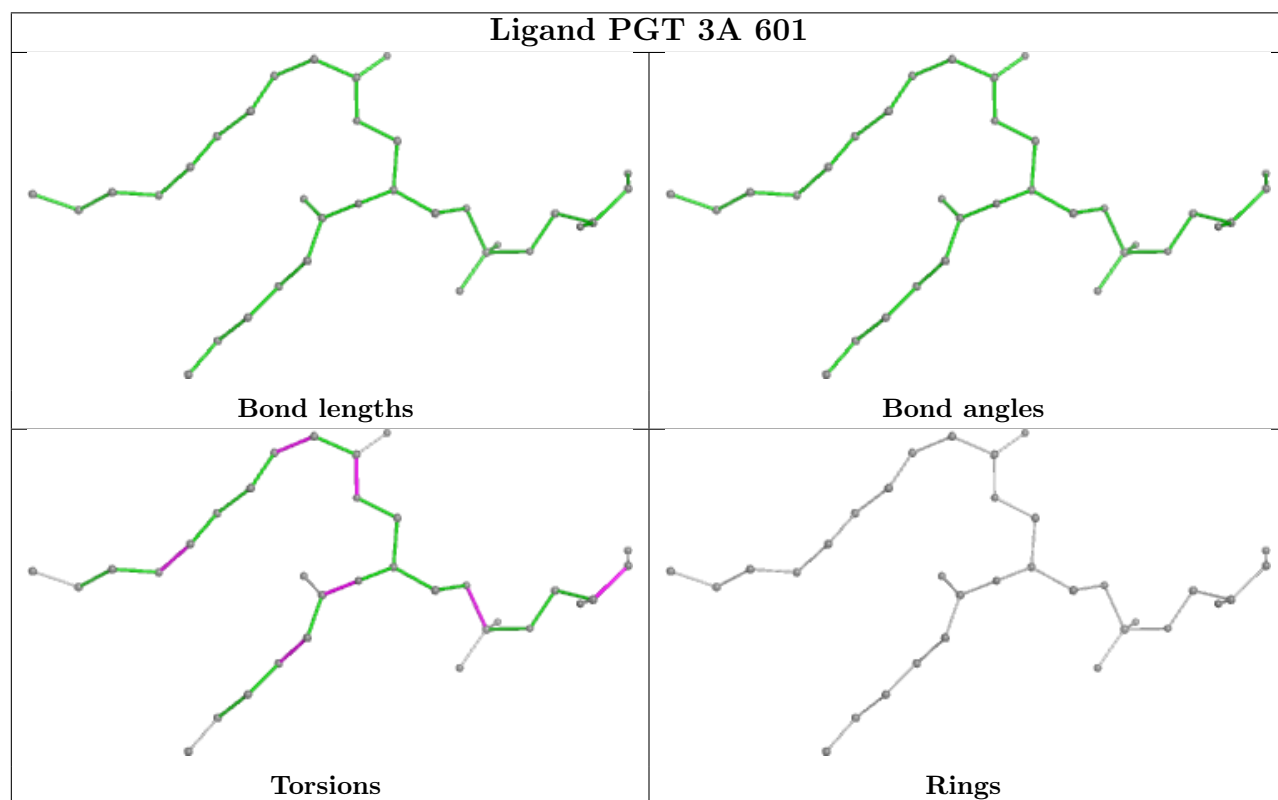
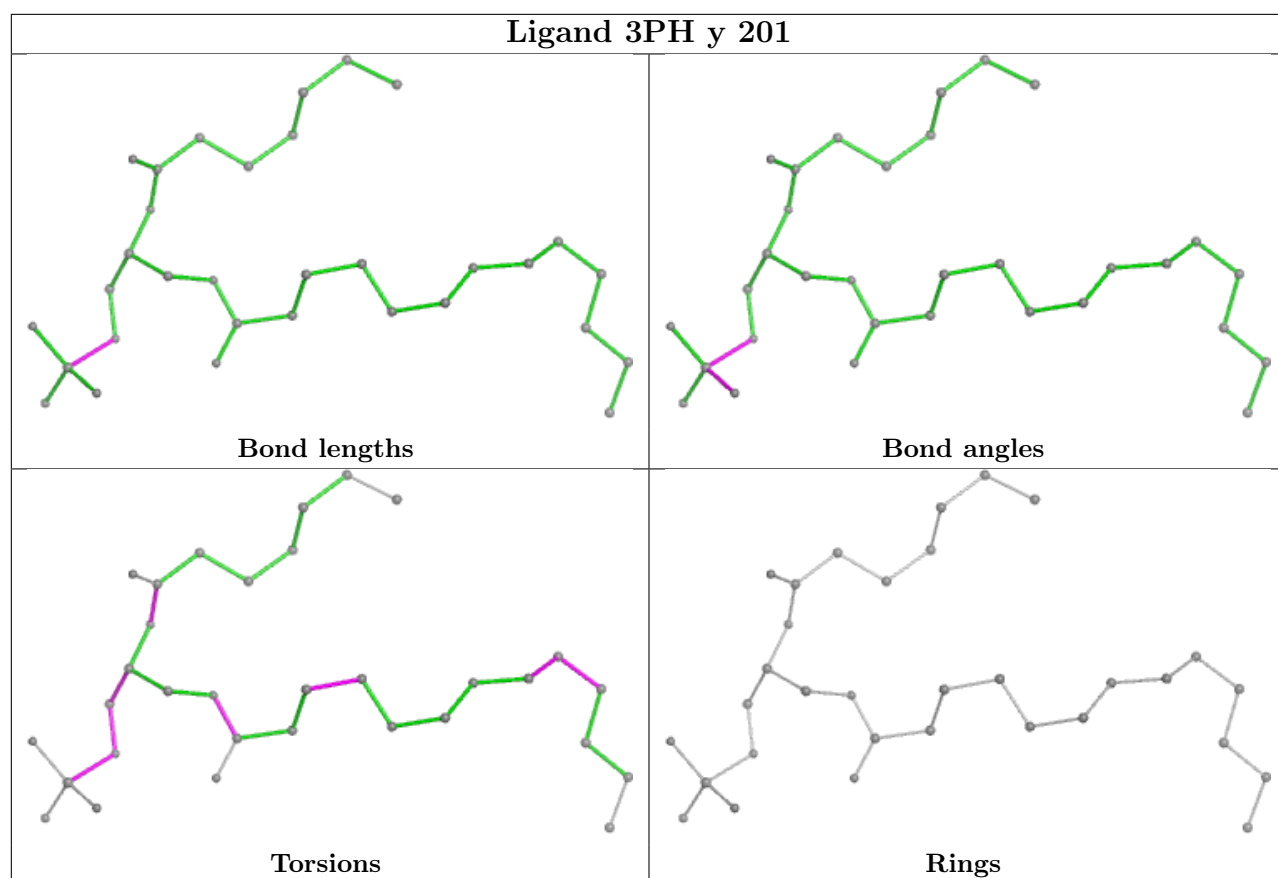


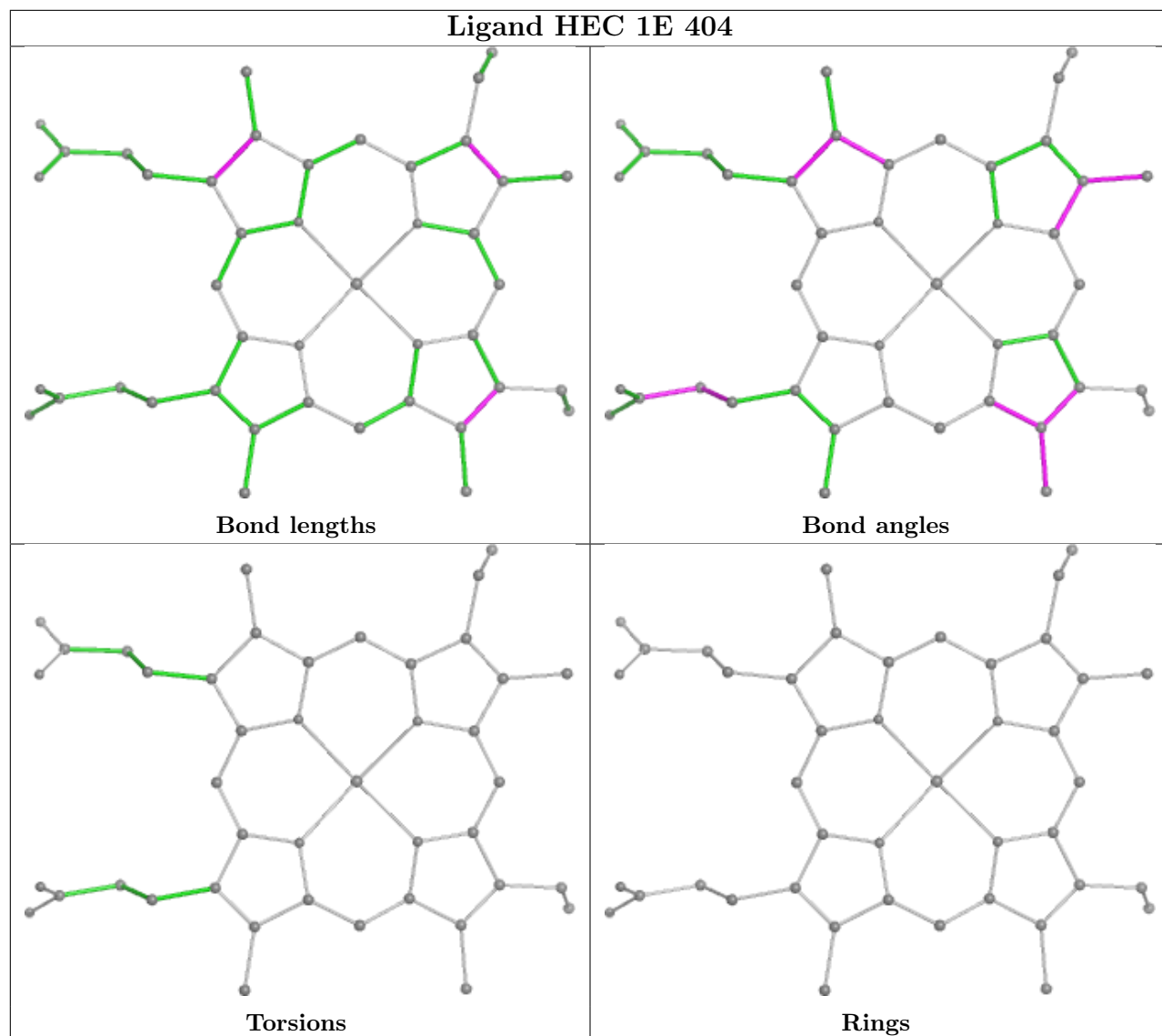


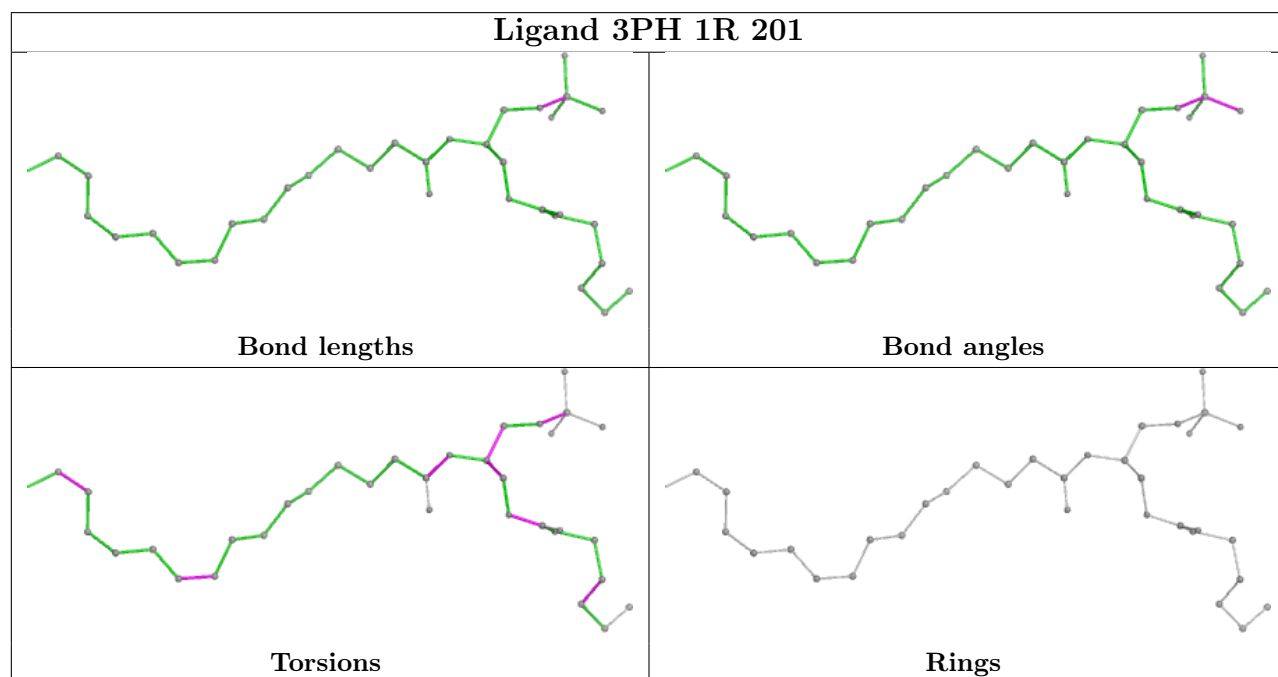
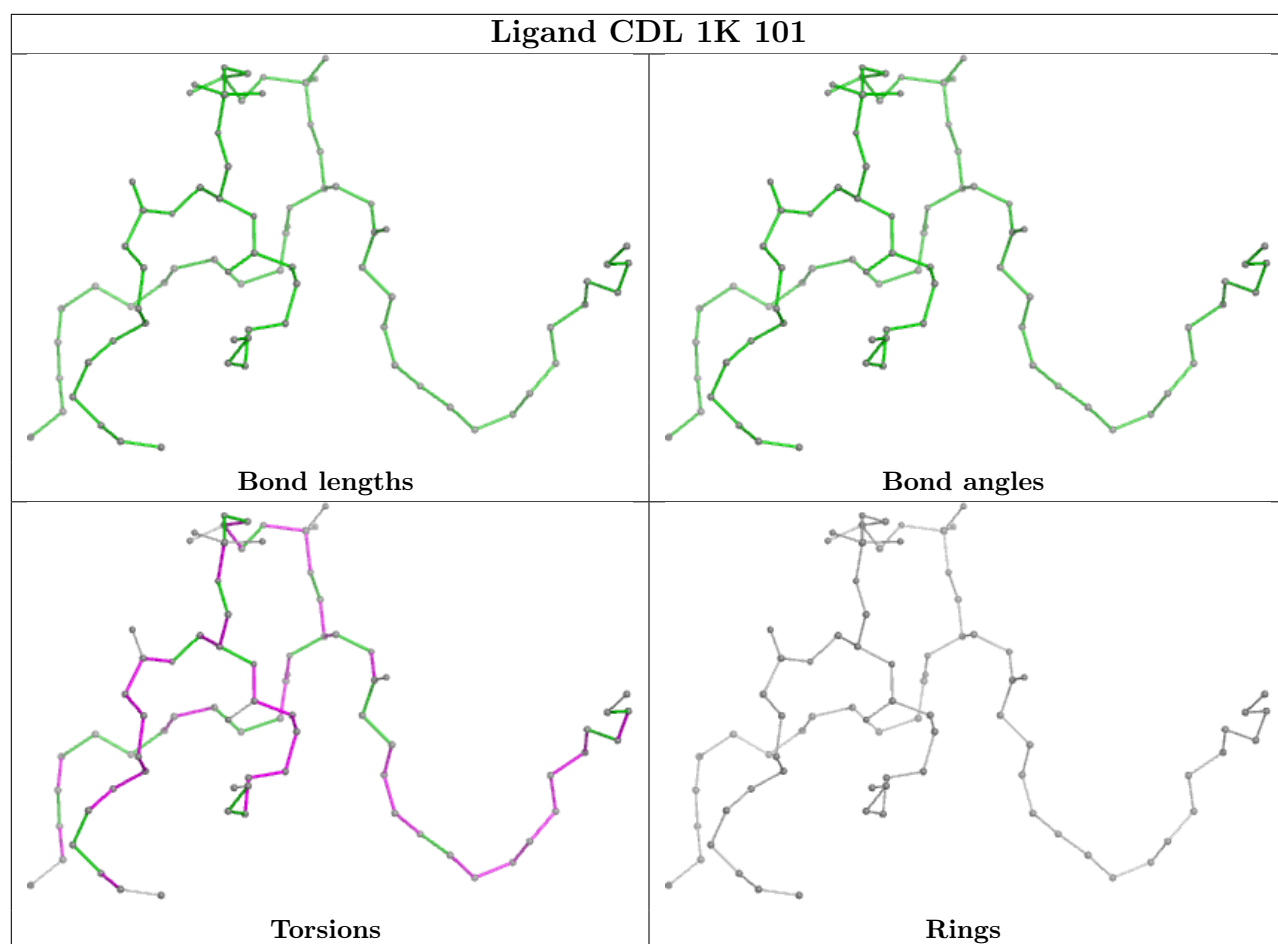


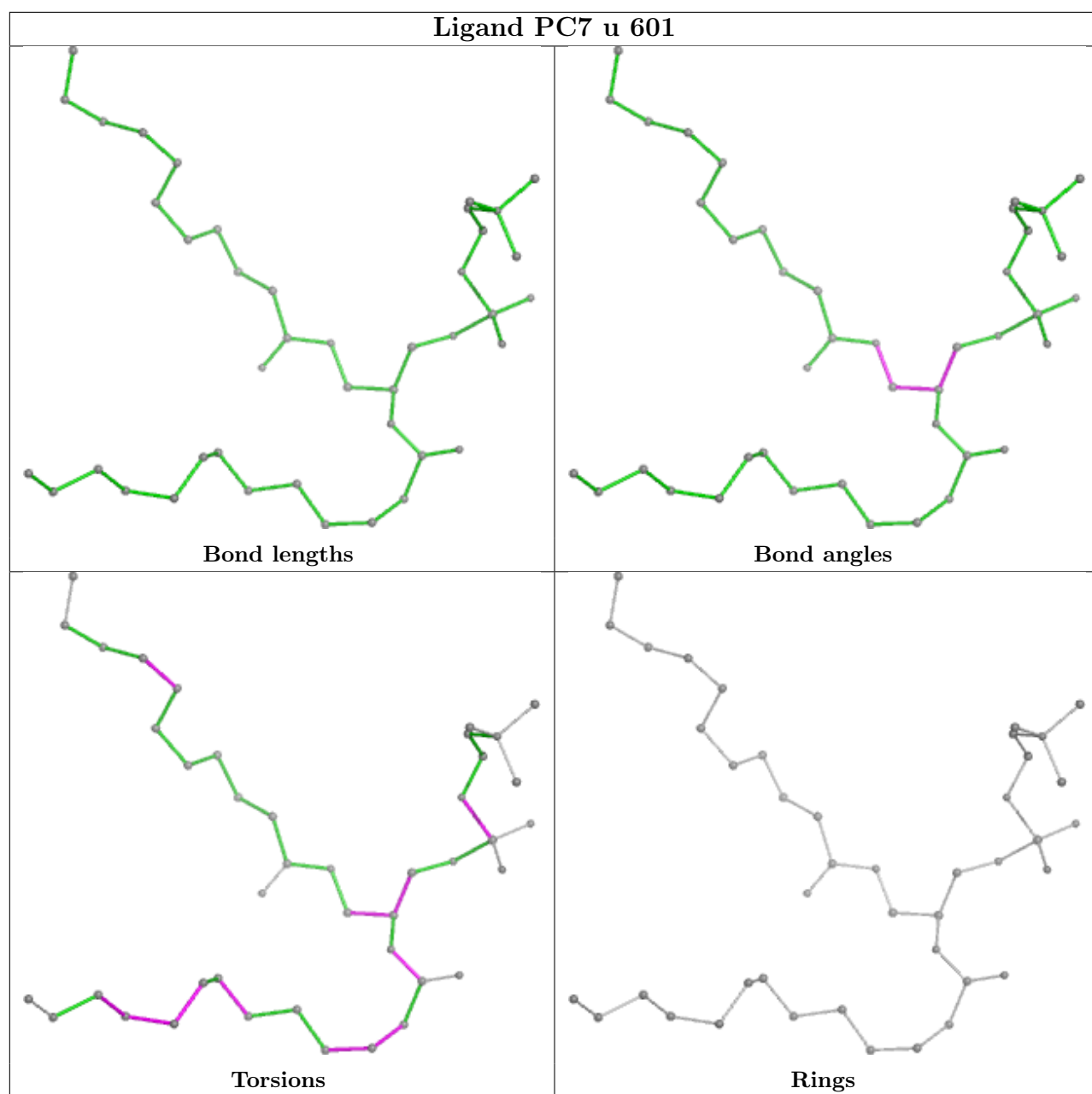


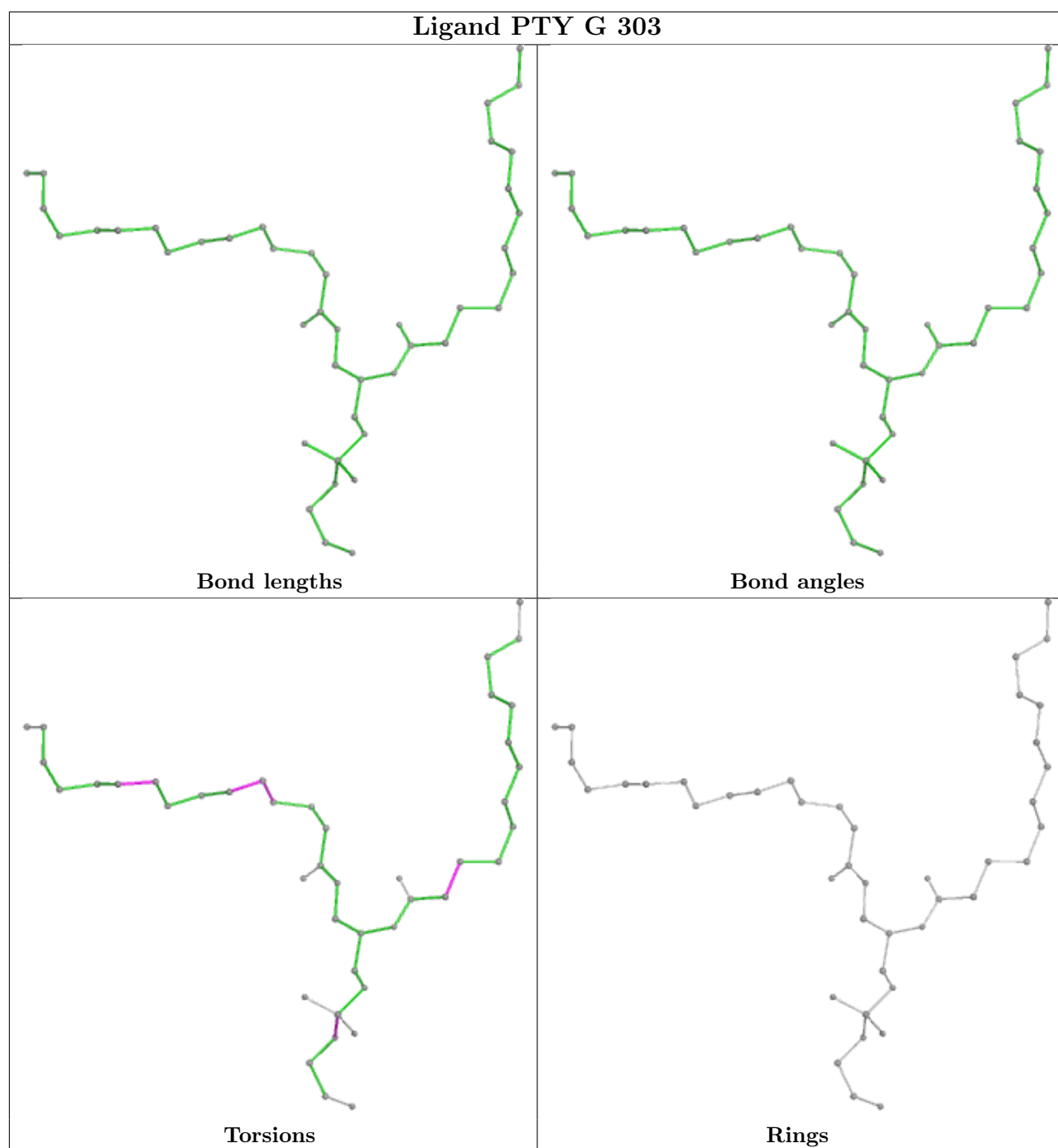


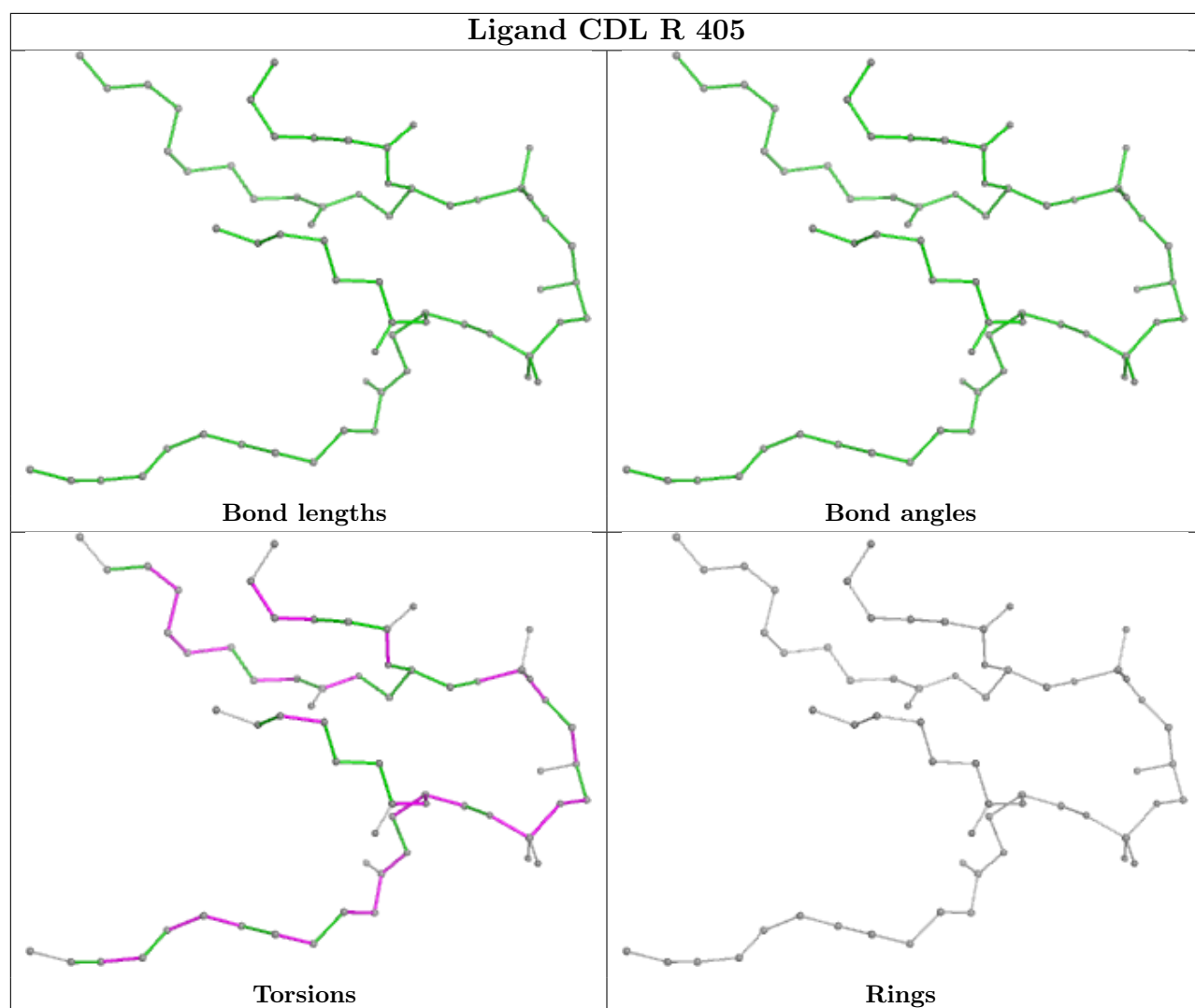


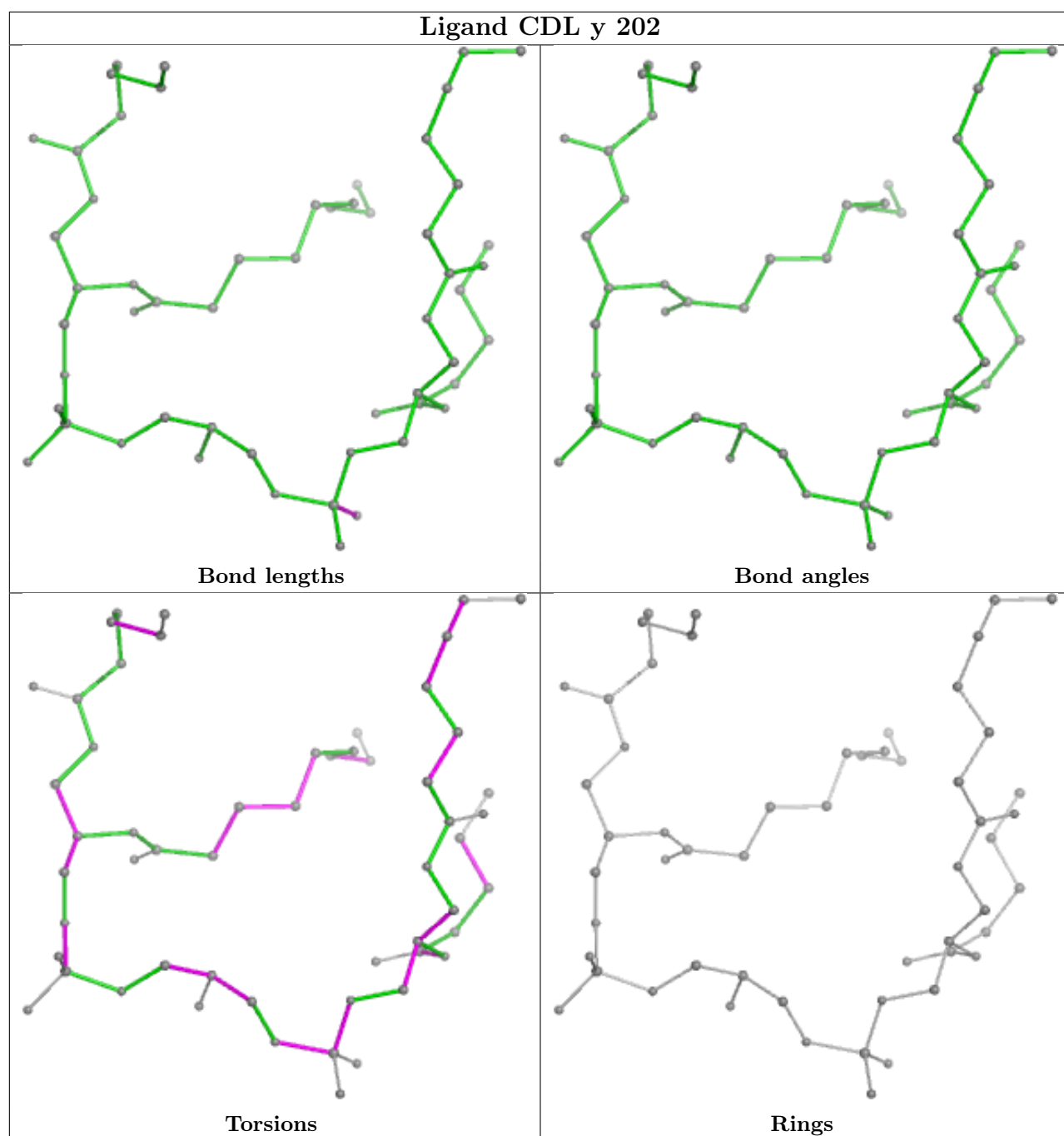


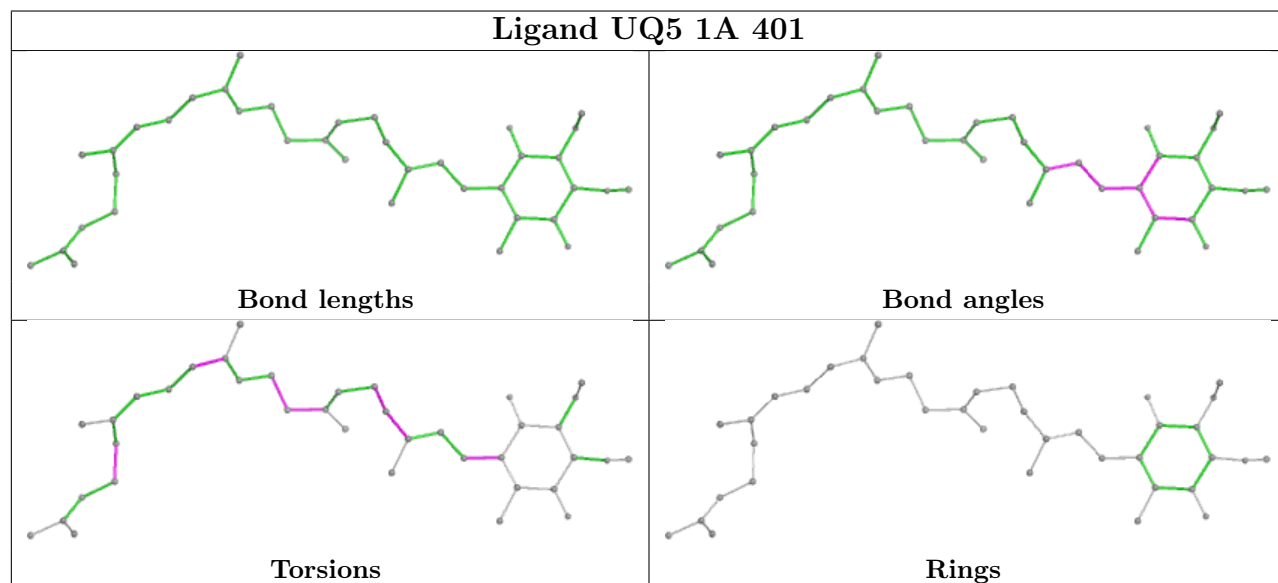
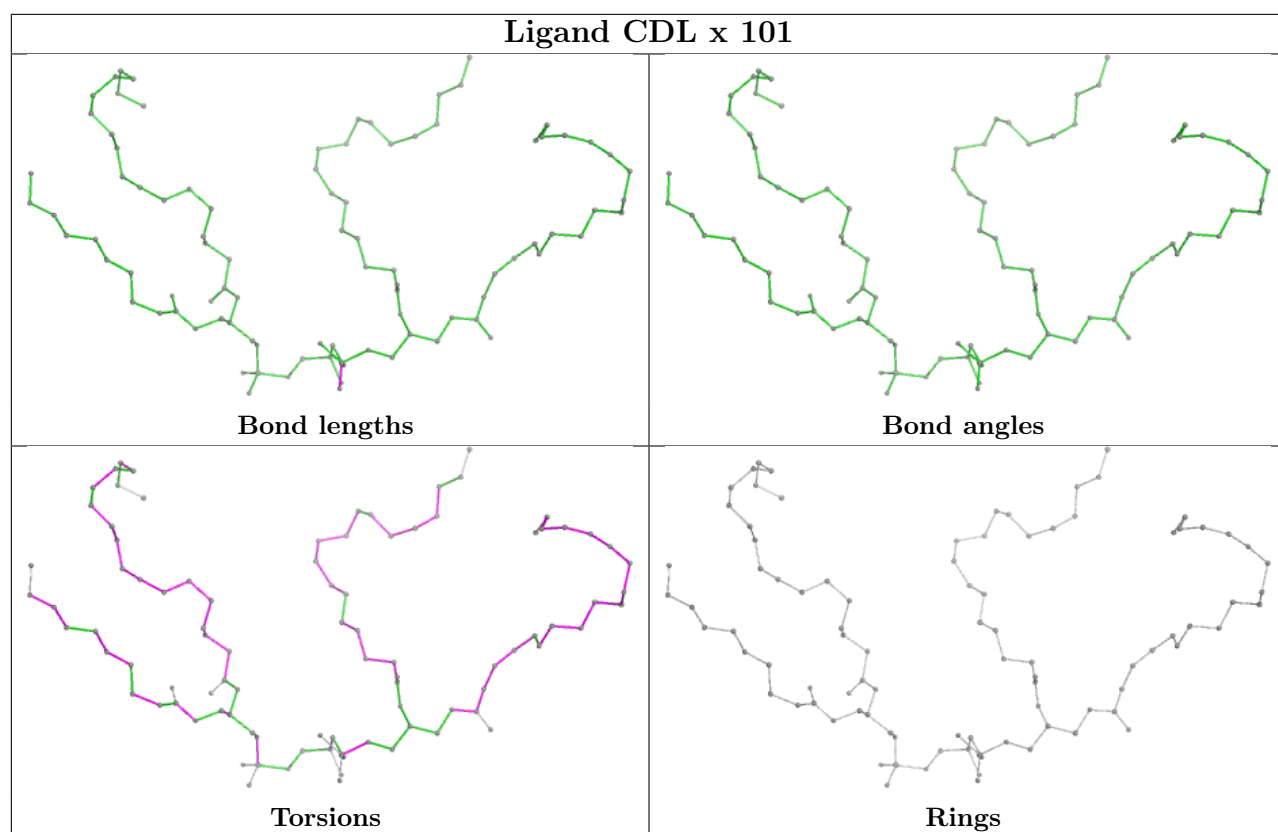


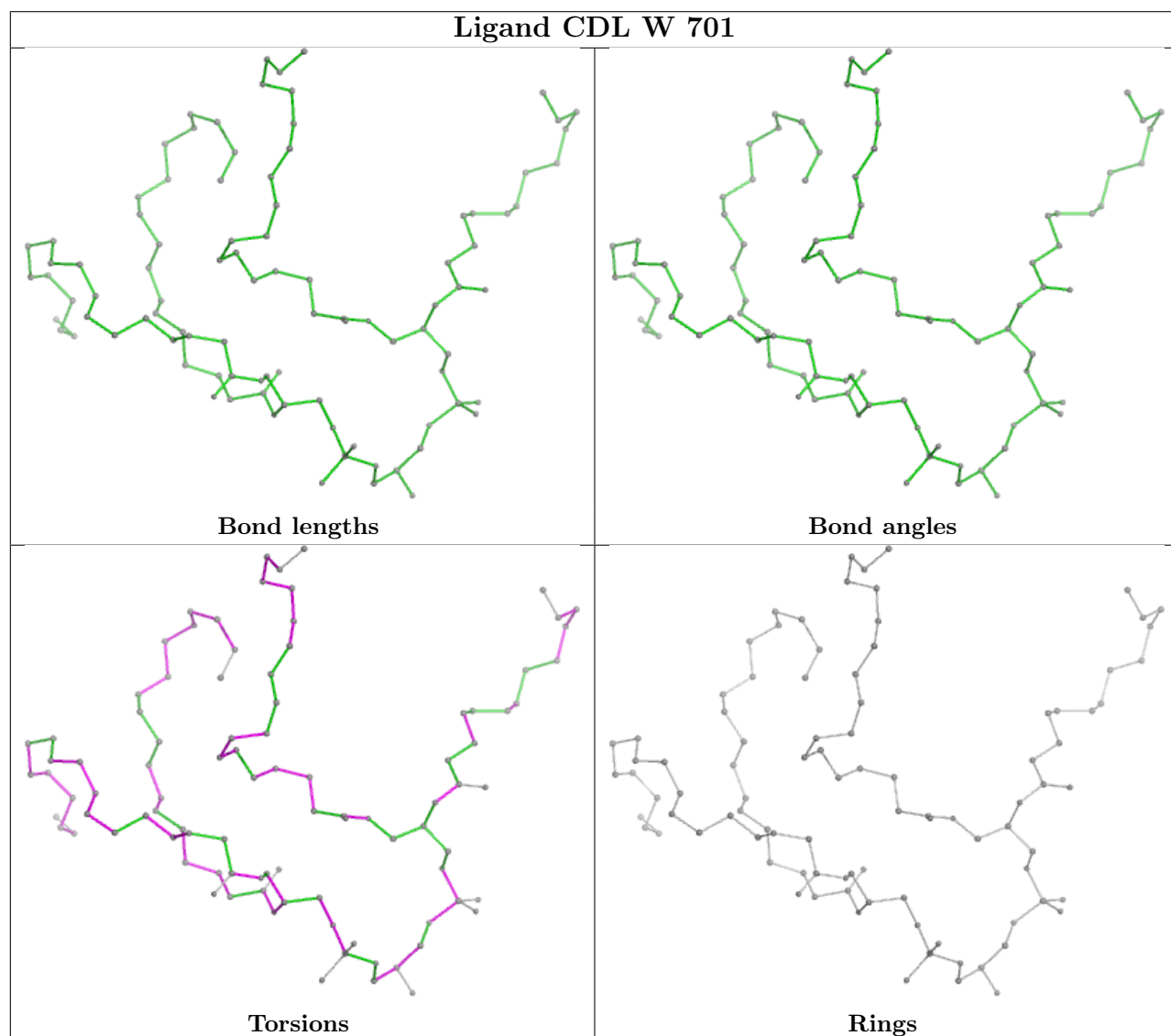
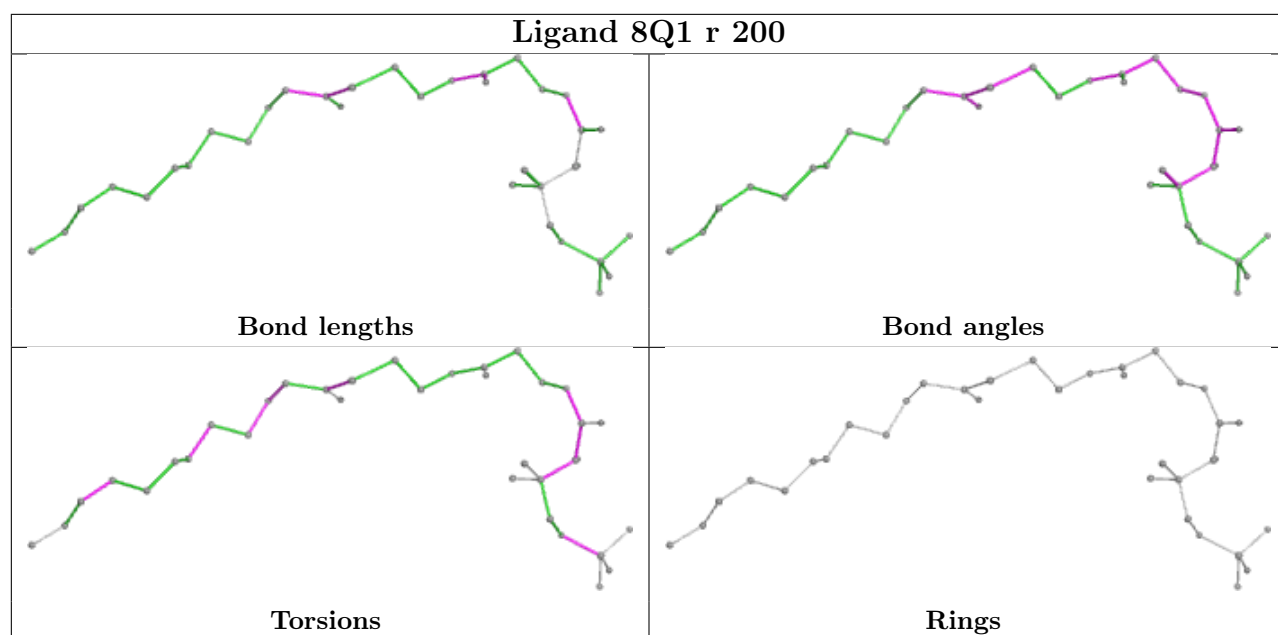


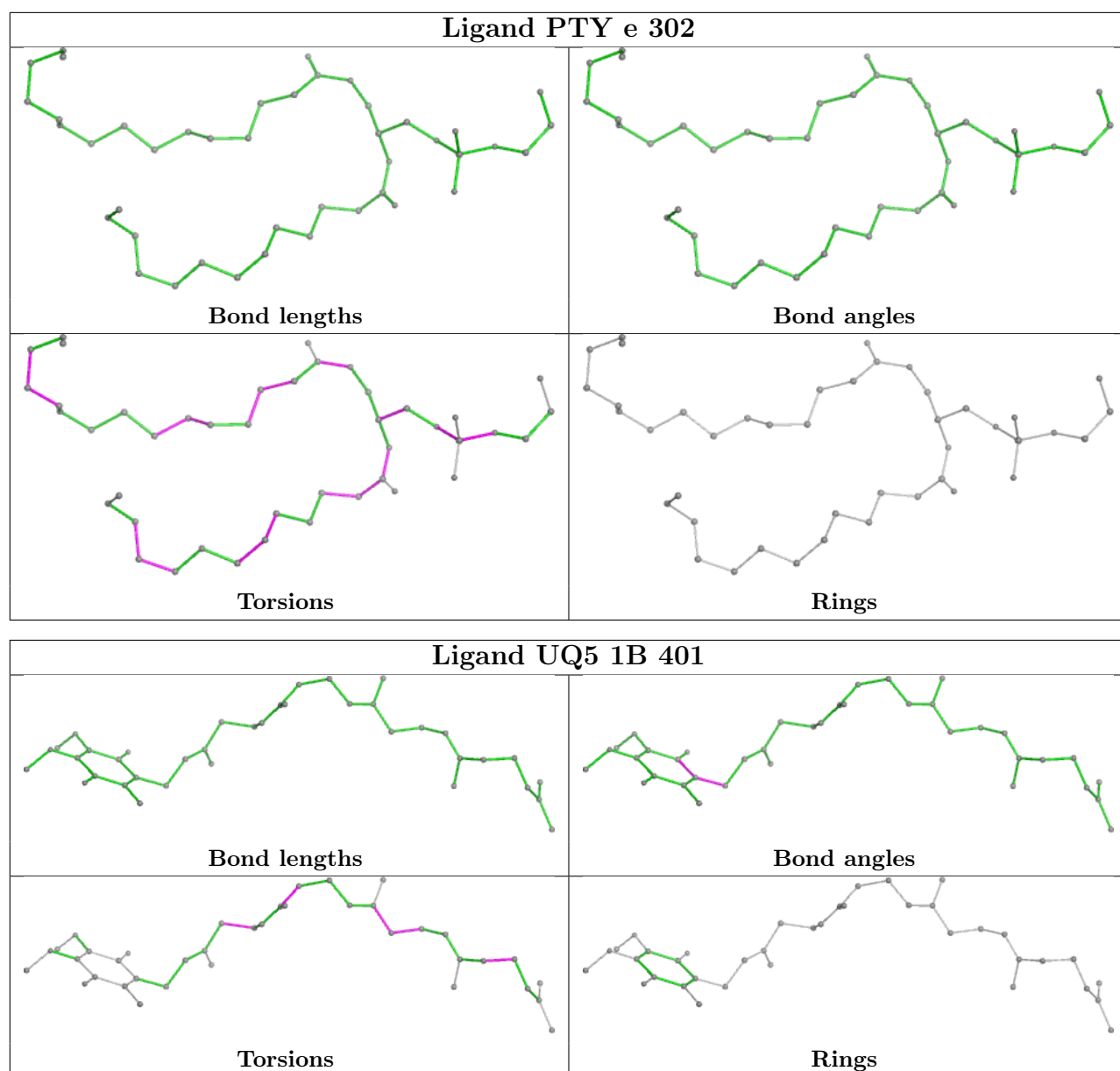


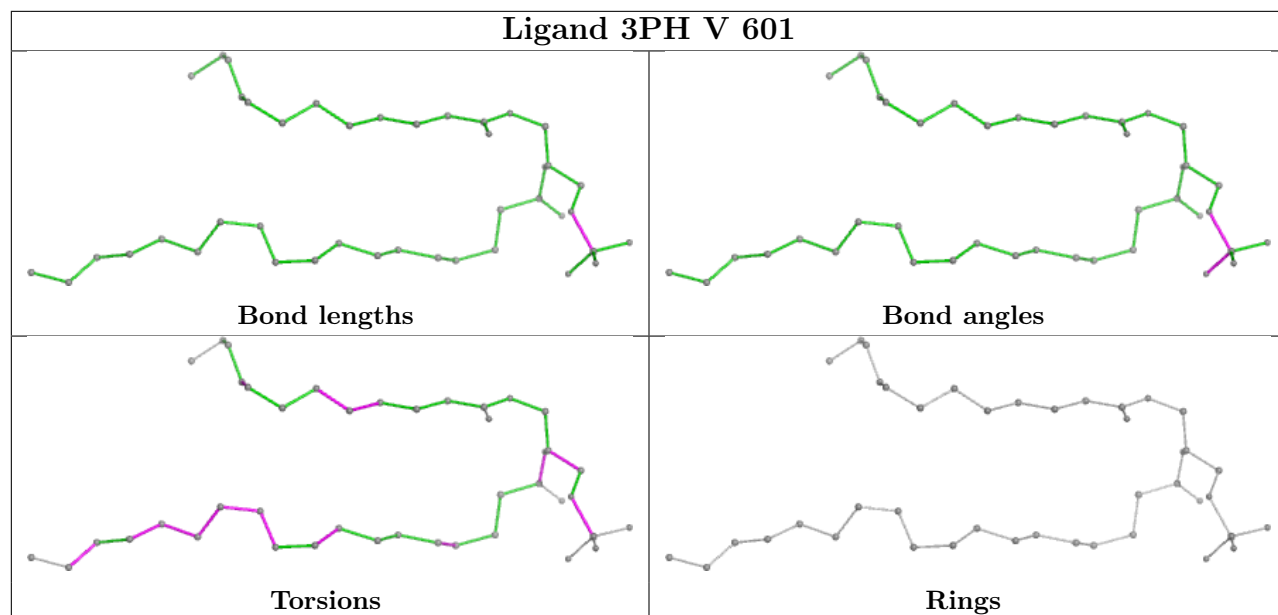
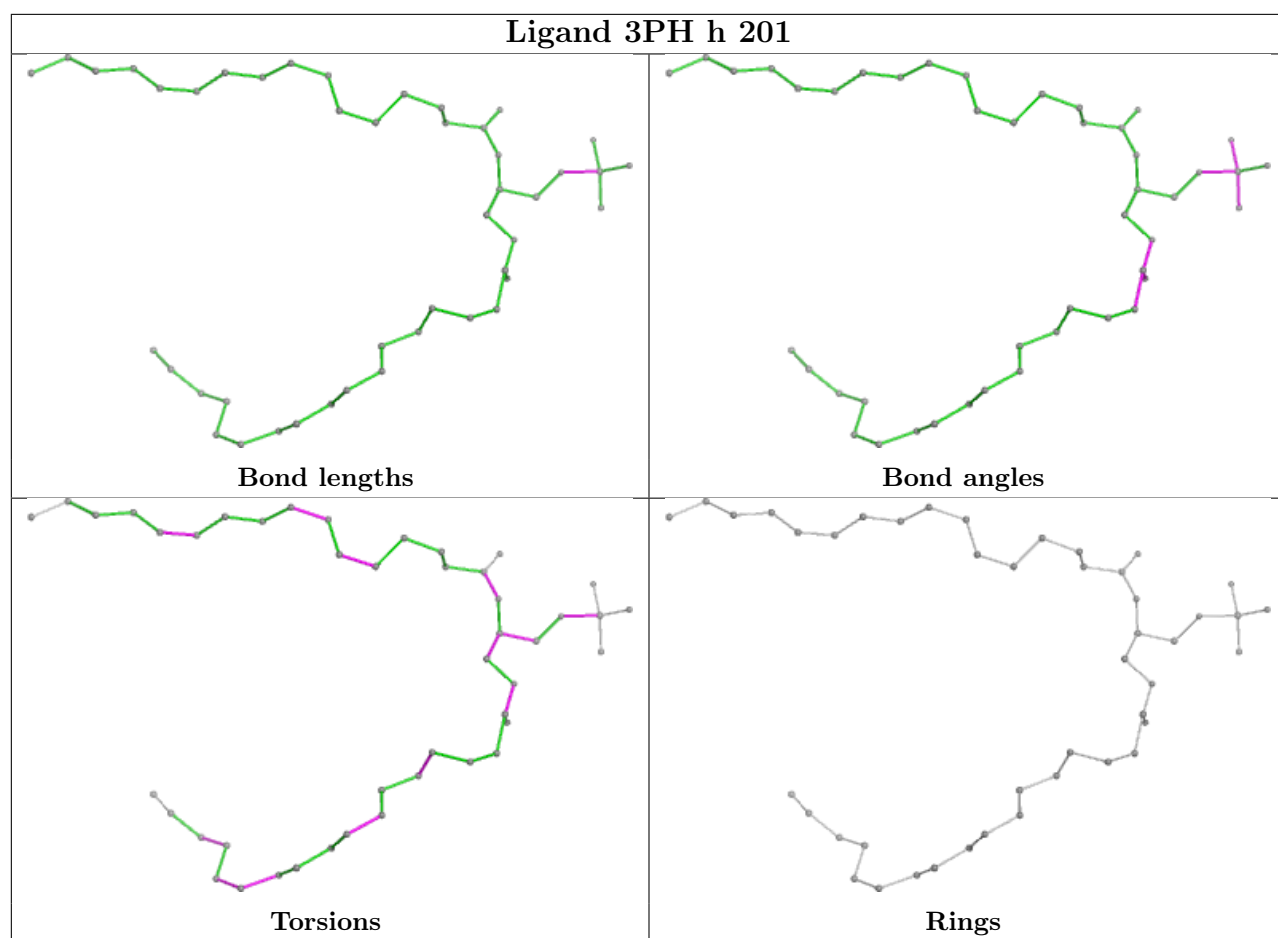


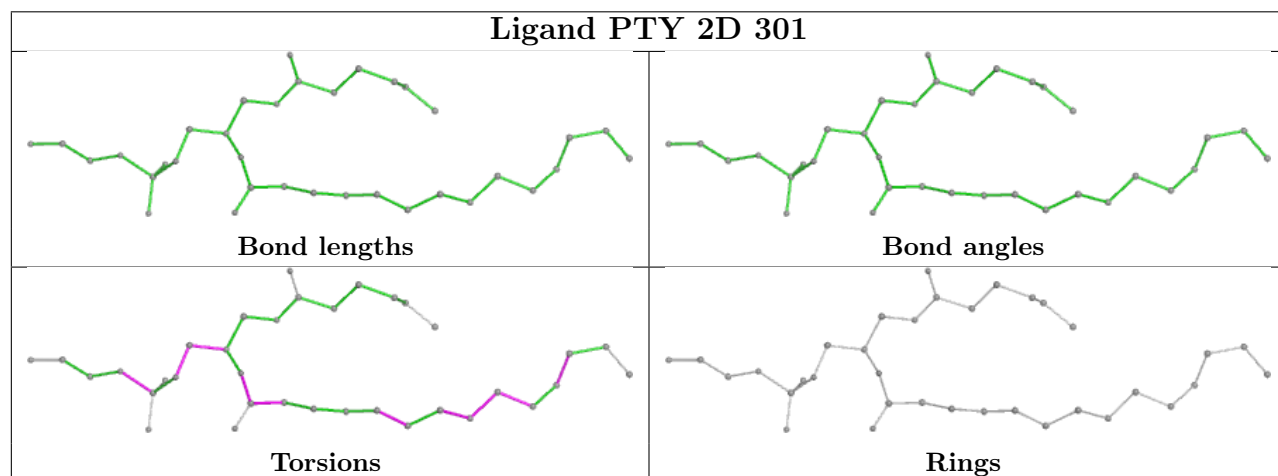
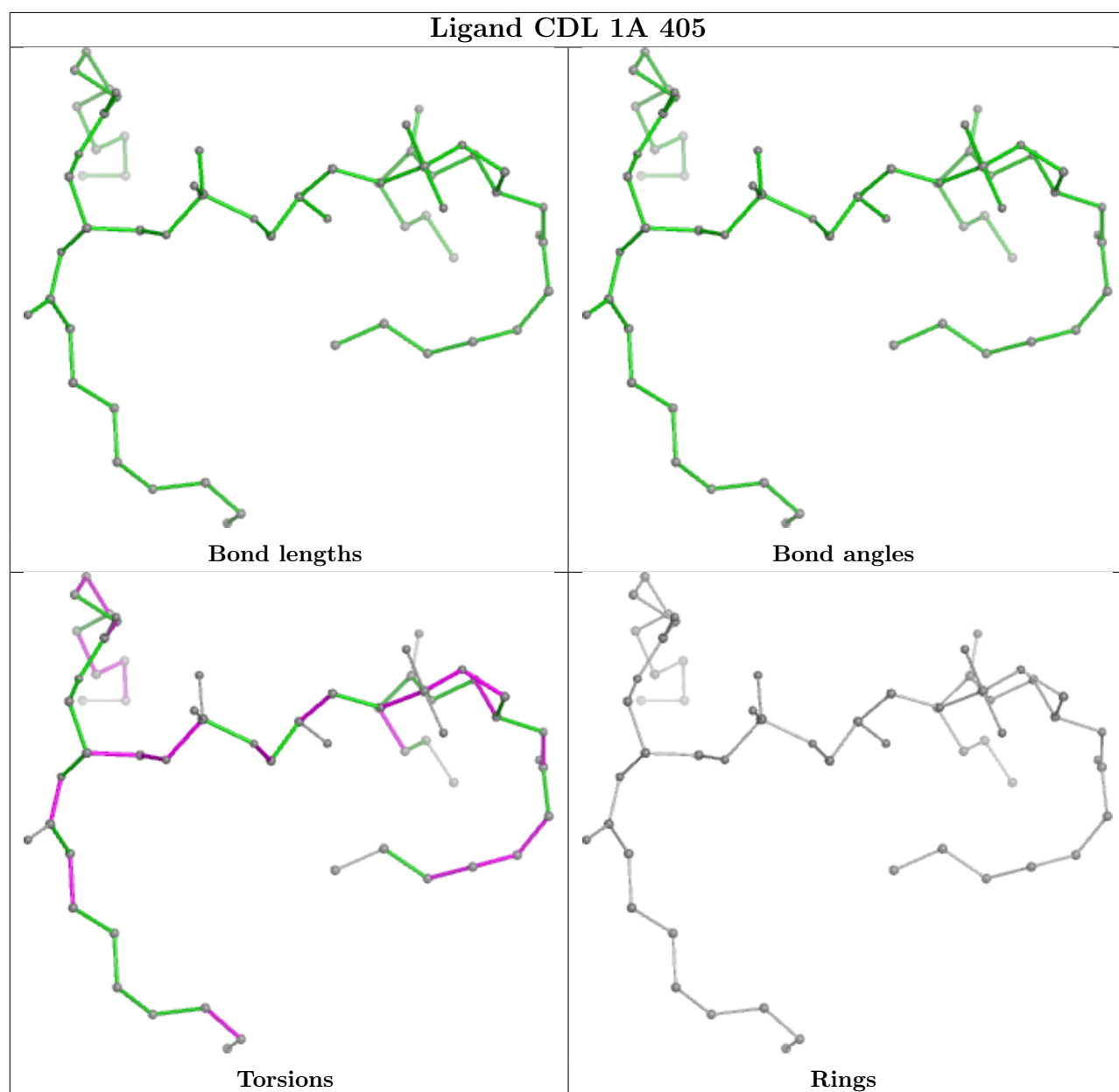


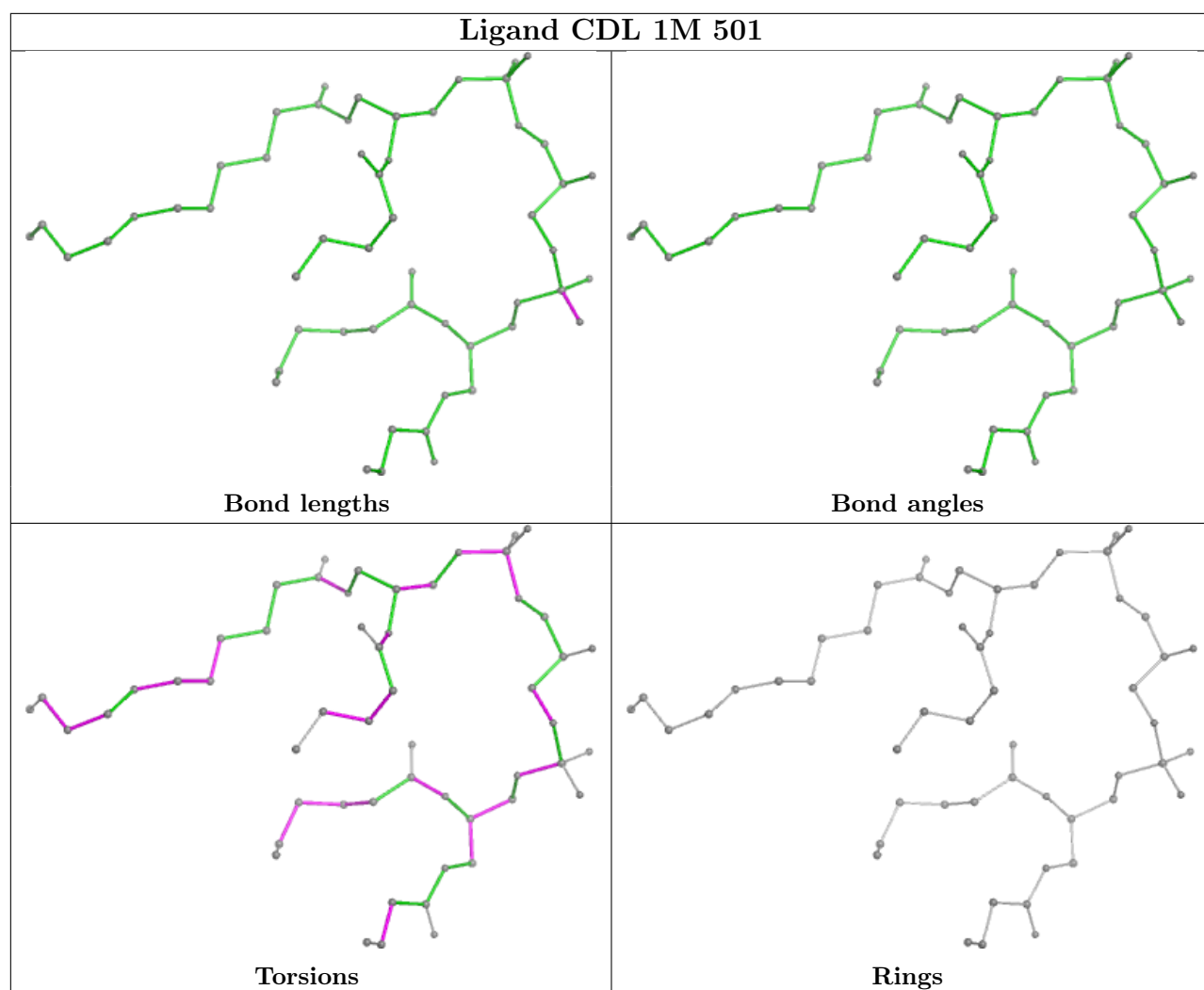


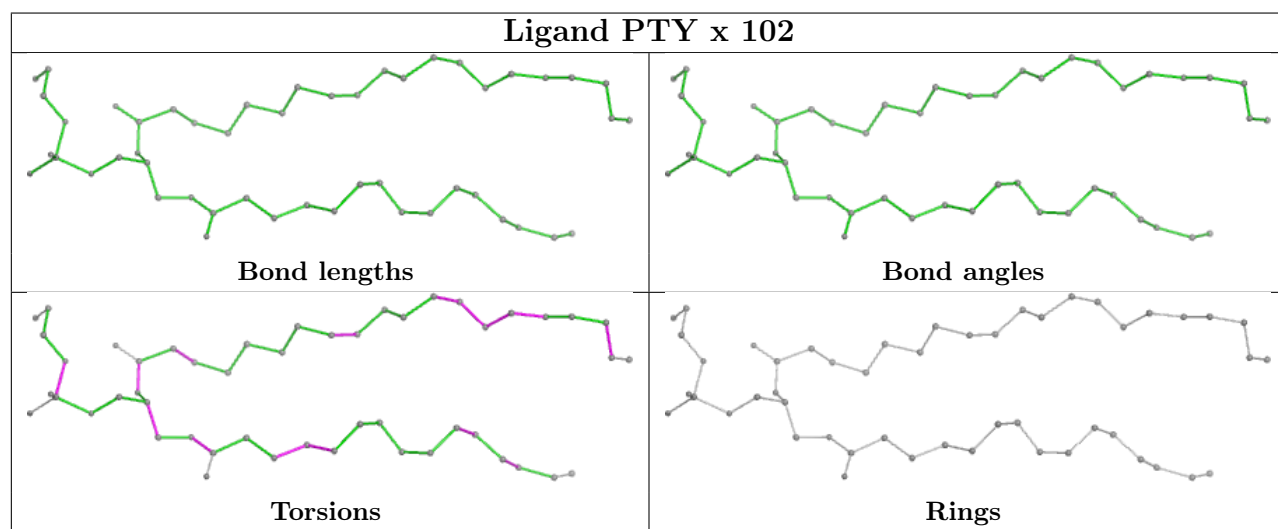
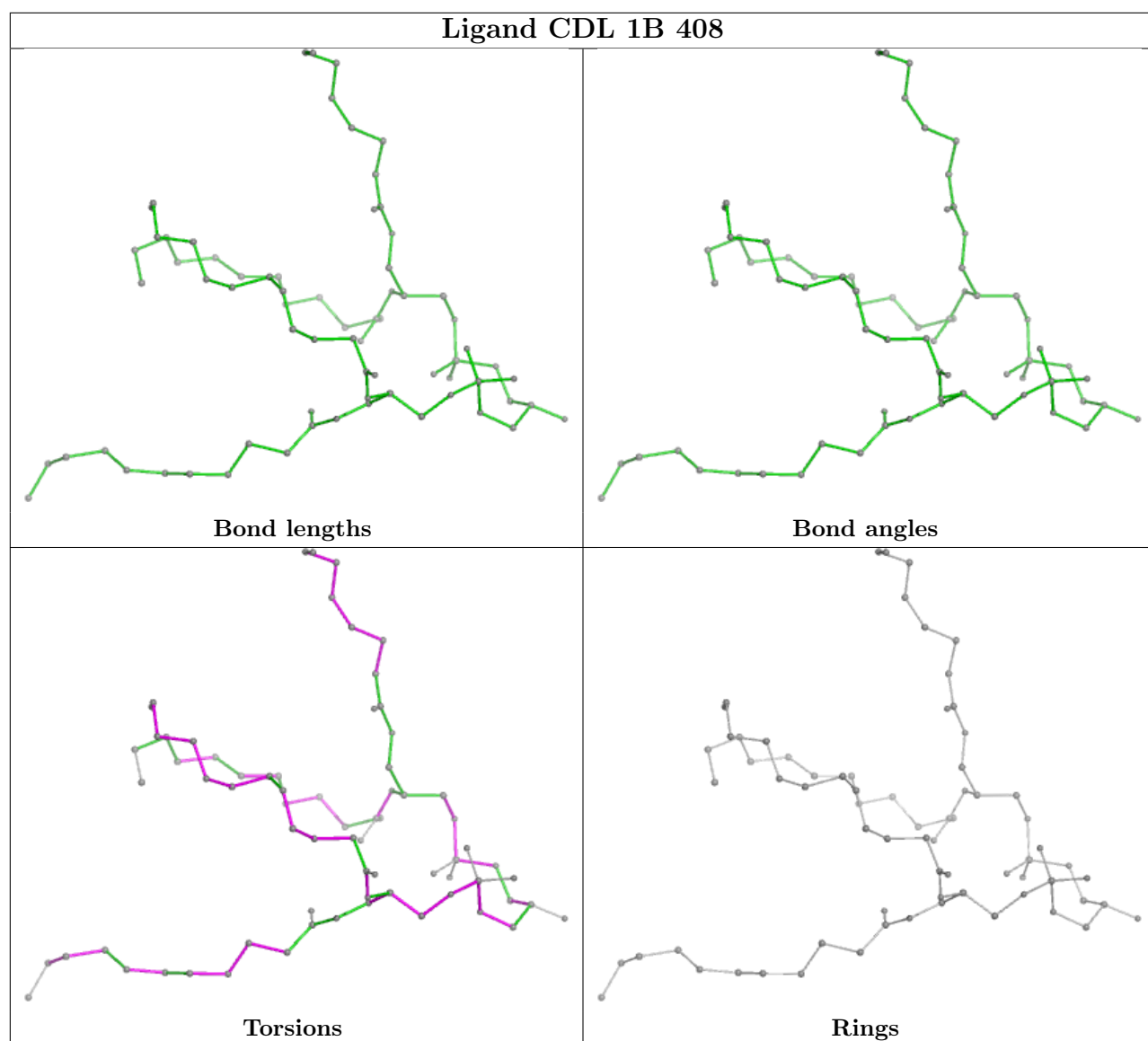


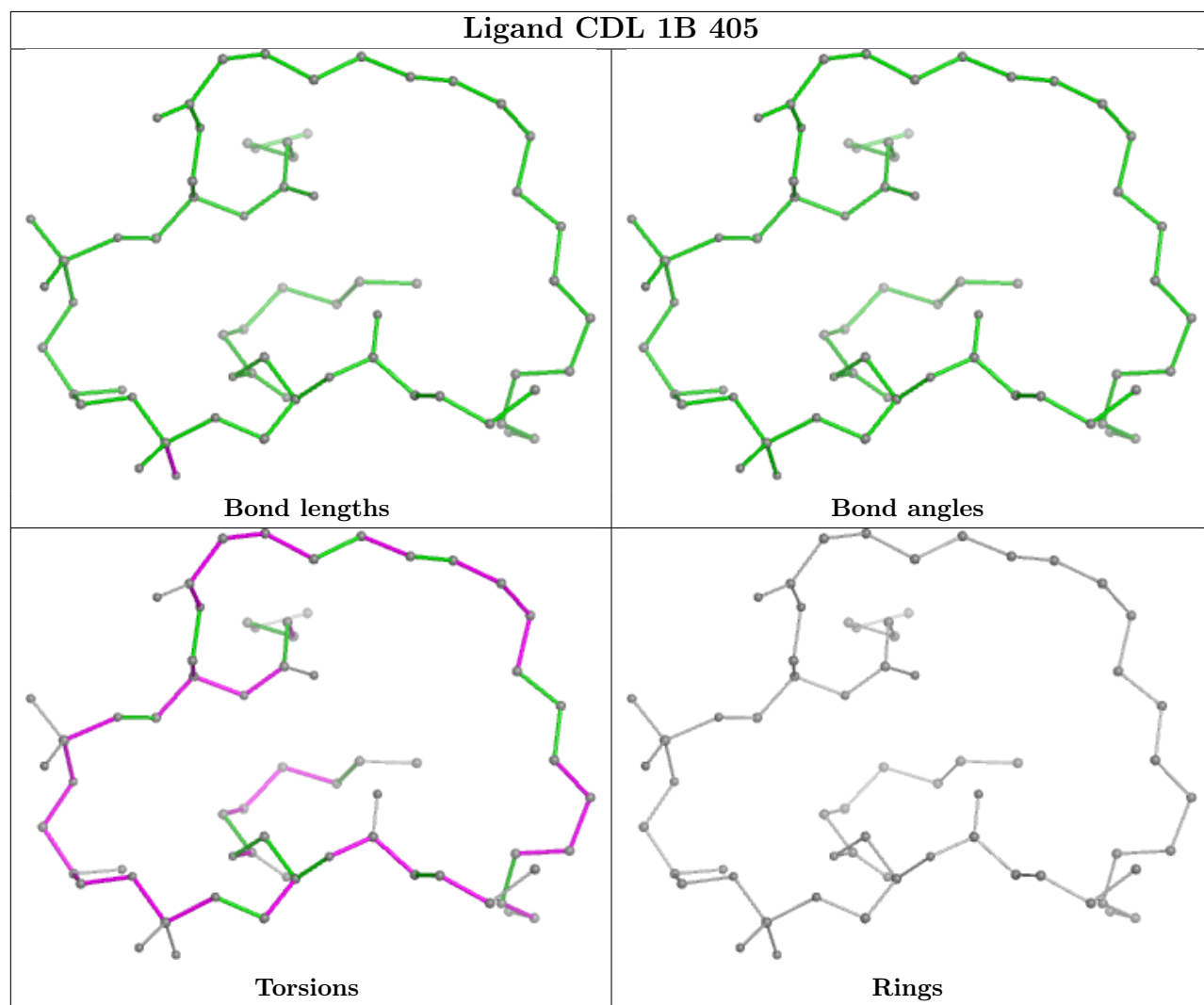
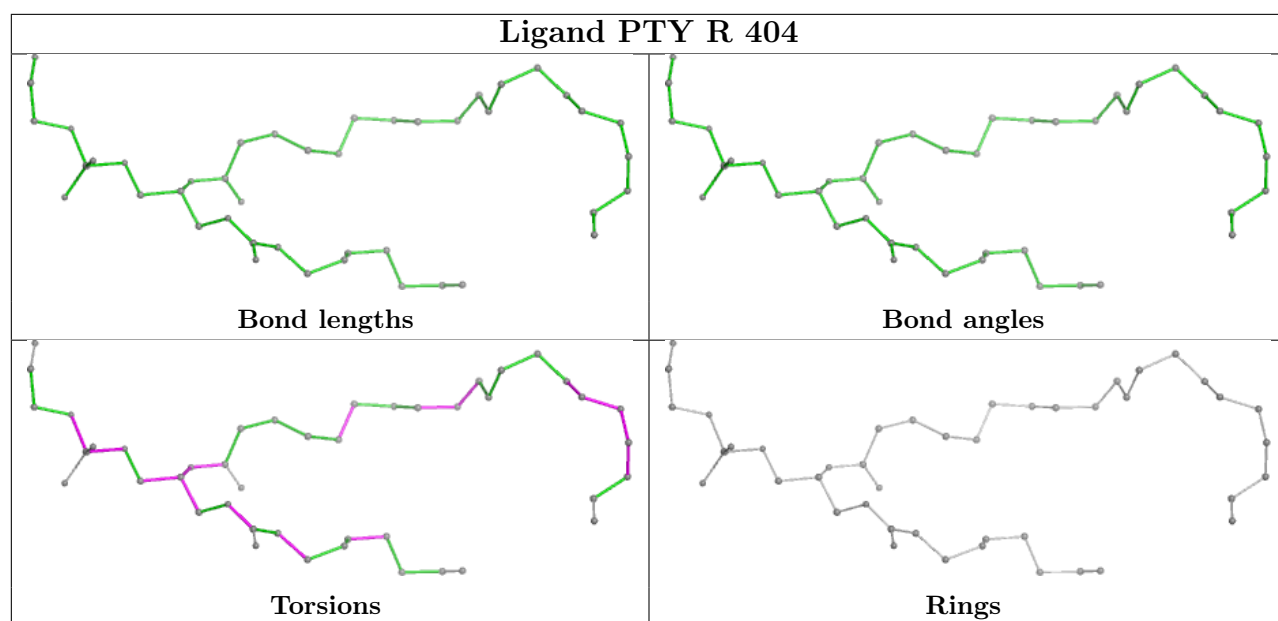


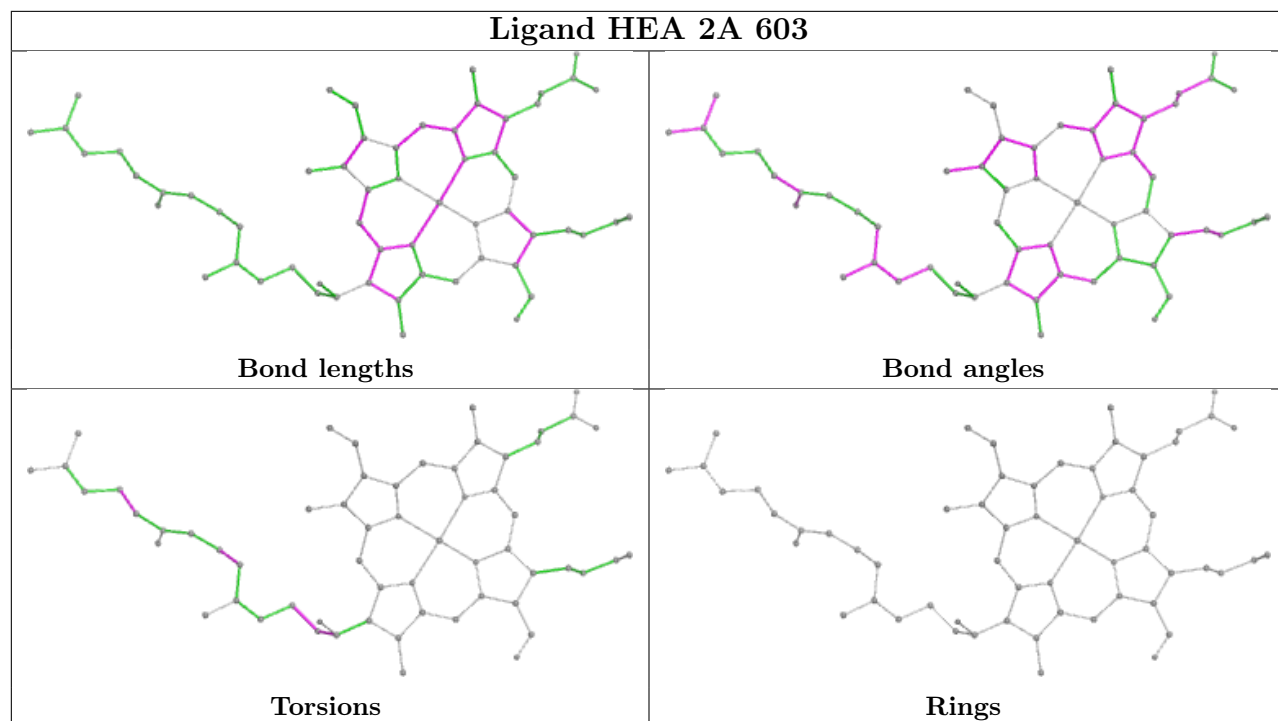
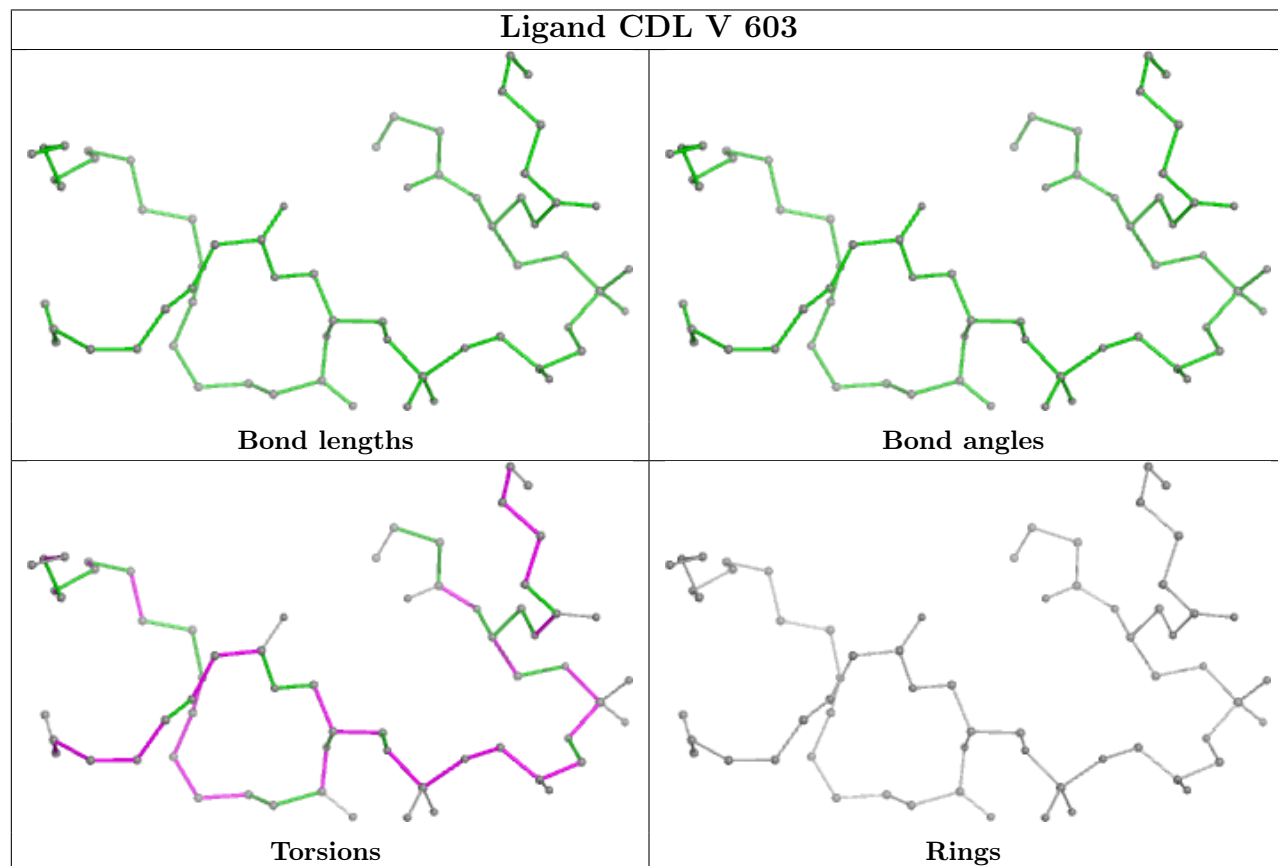


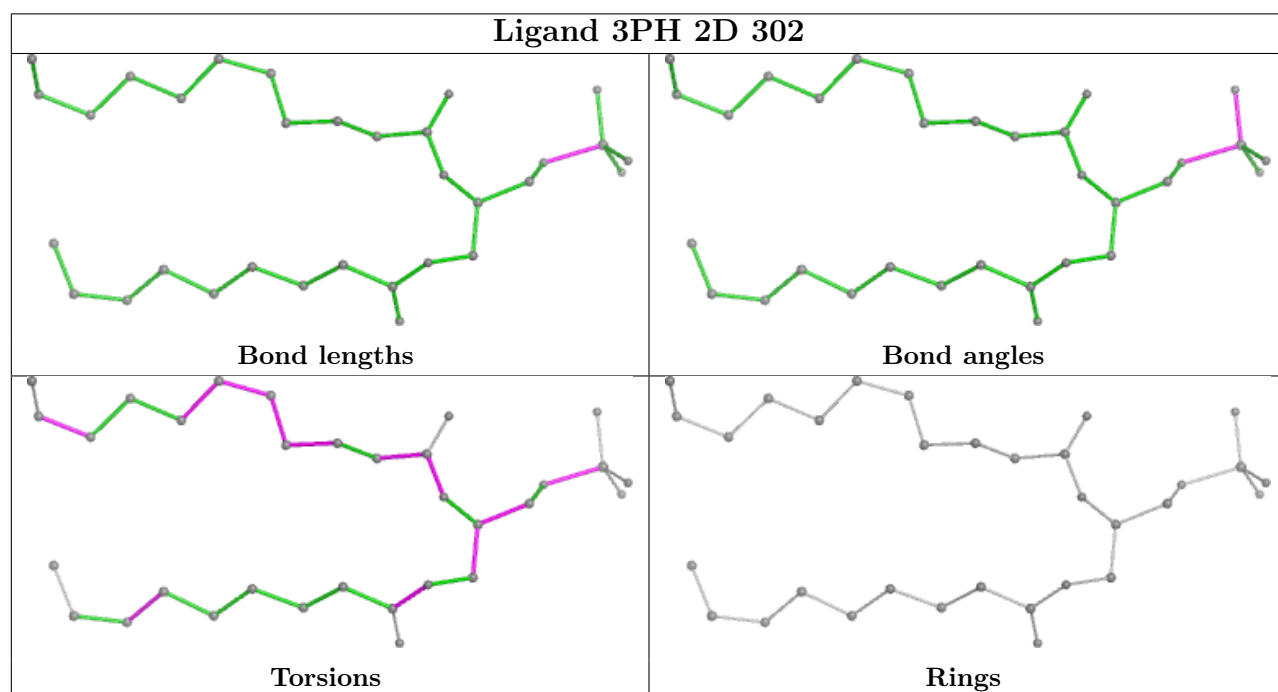
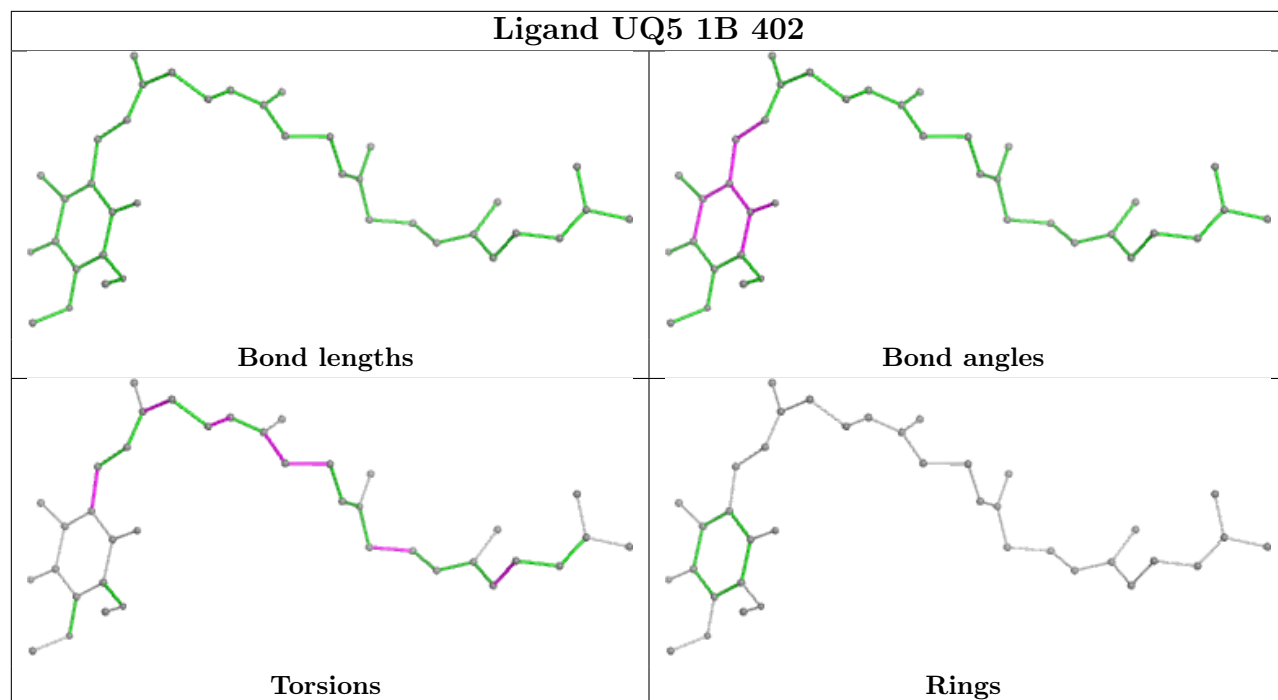


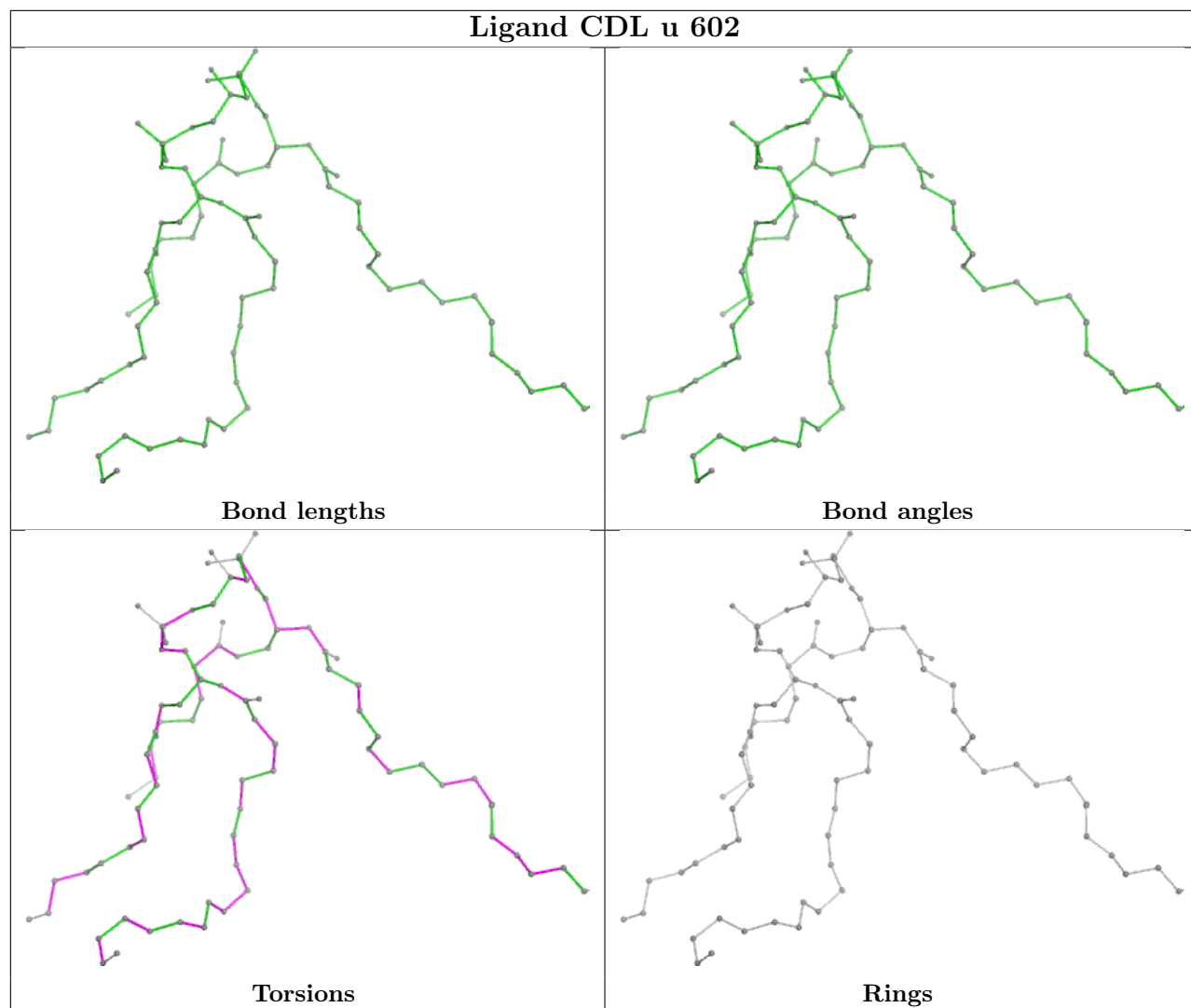


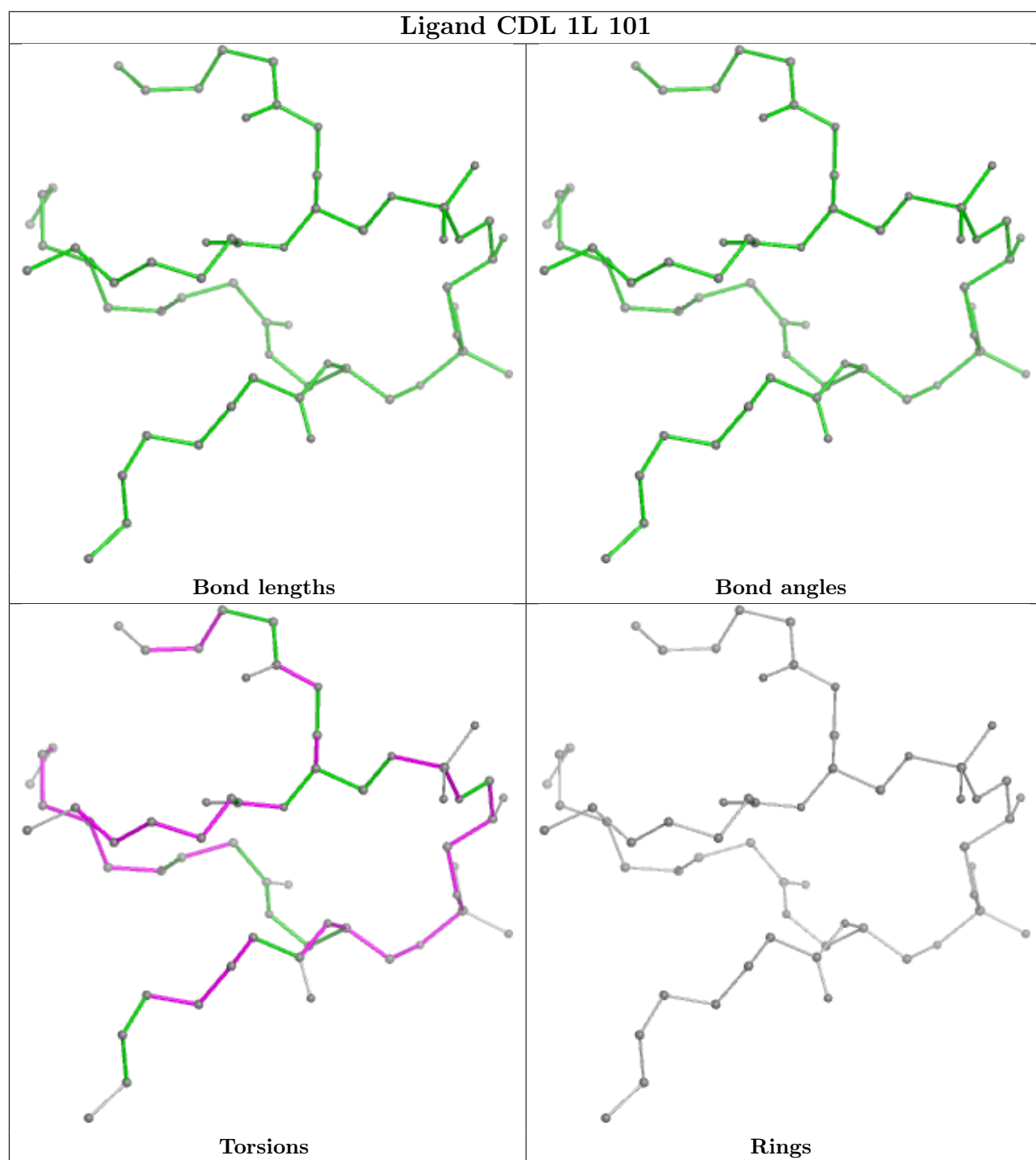


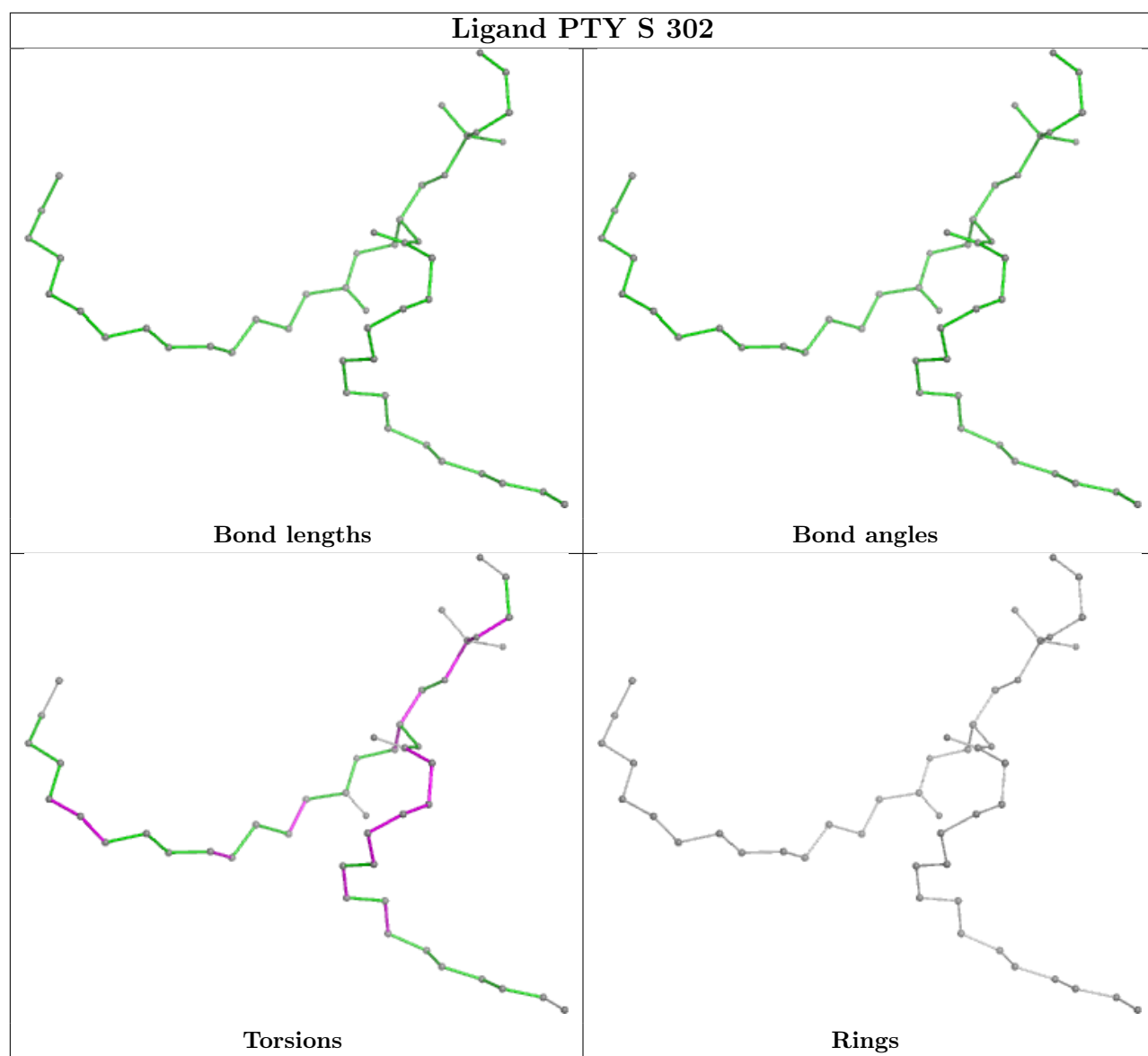


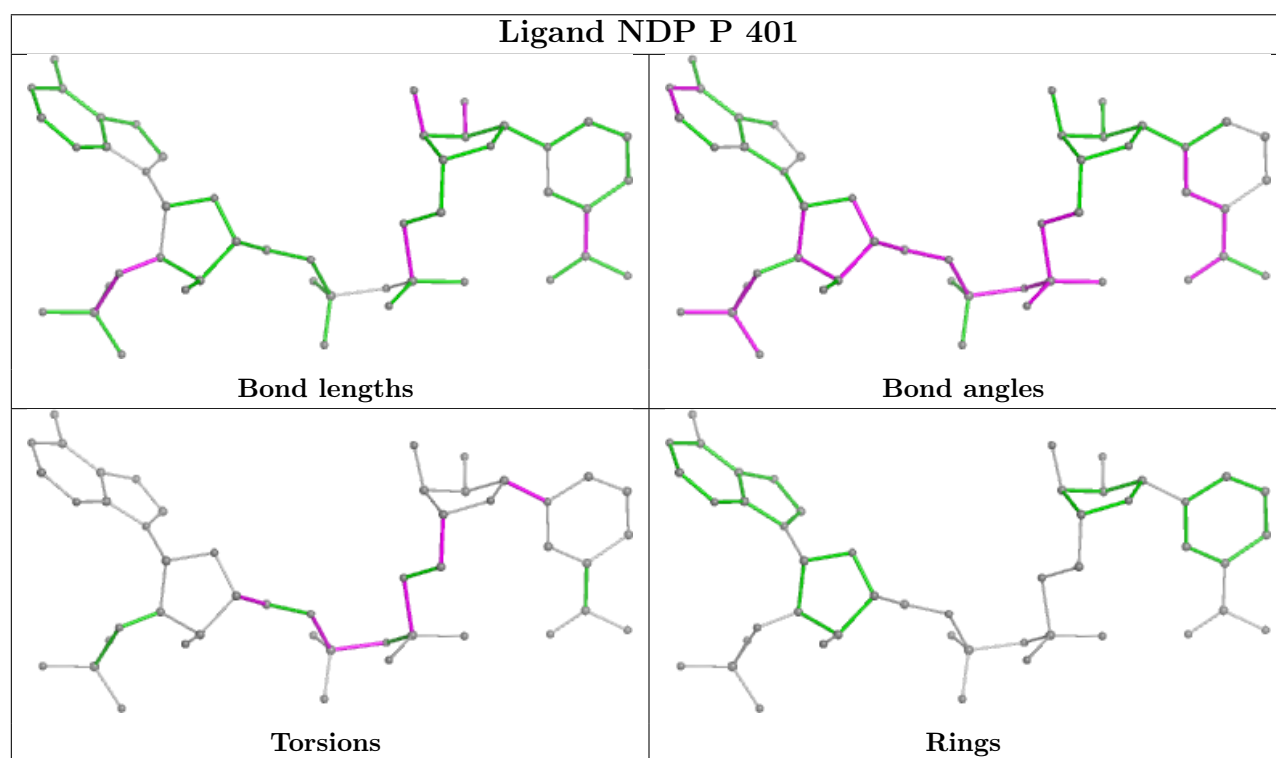
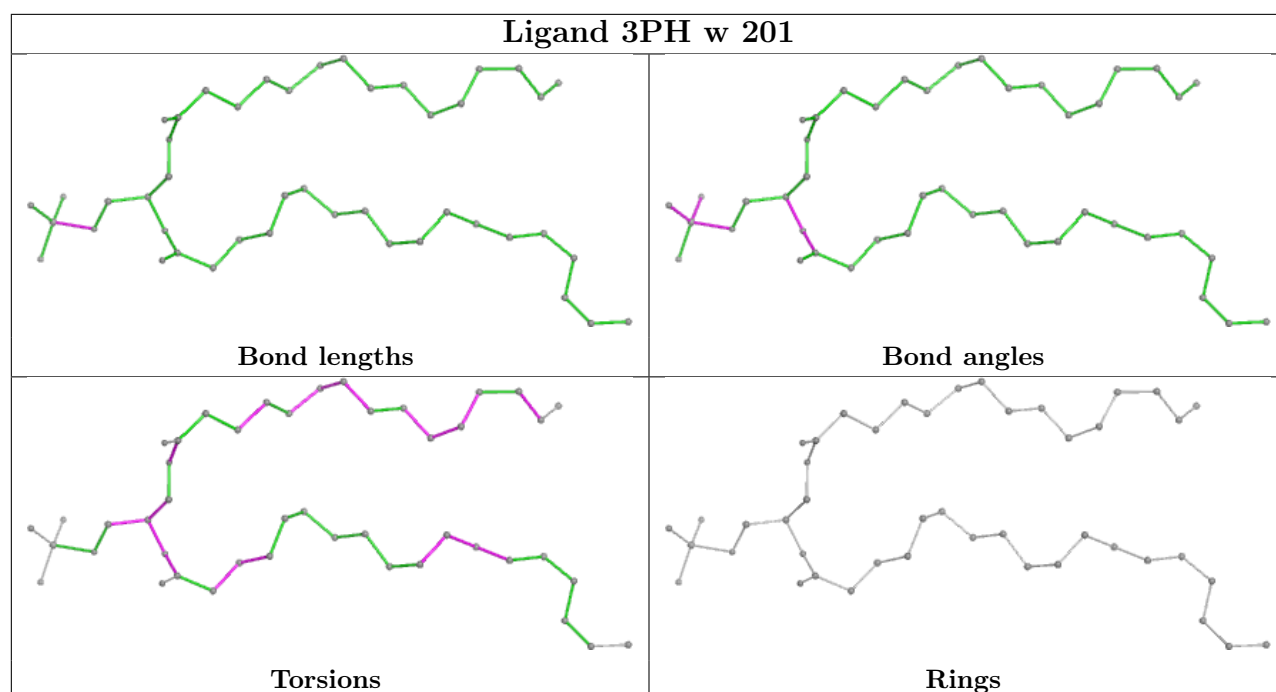
Ligand HEA 2A 603**Ligand CDL V 603**



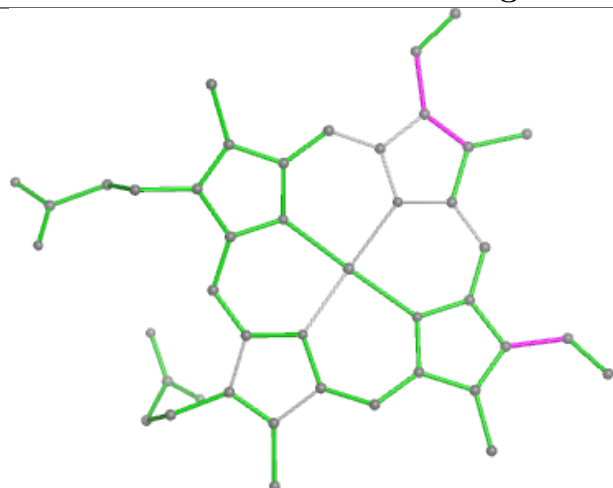




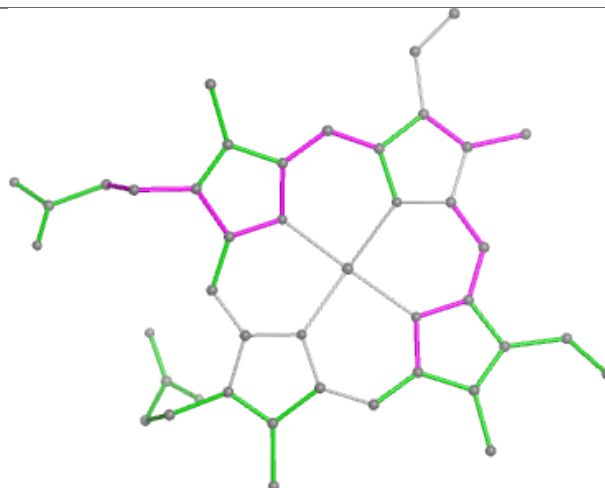




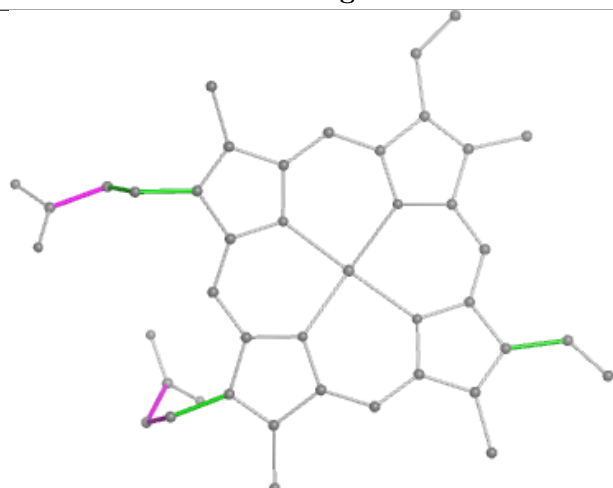
Ligand HEM 1B 404



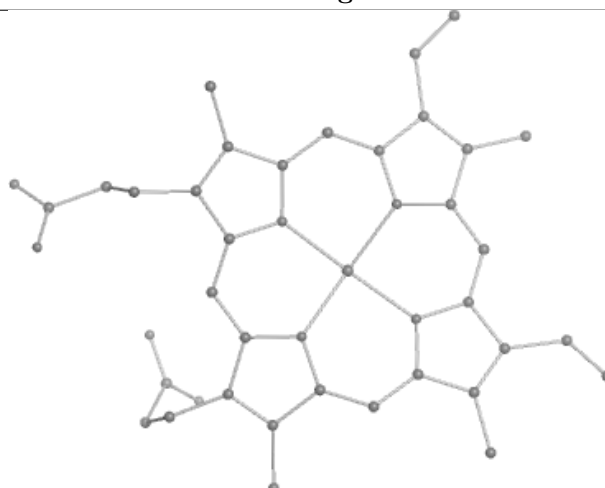
Bond lengths



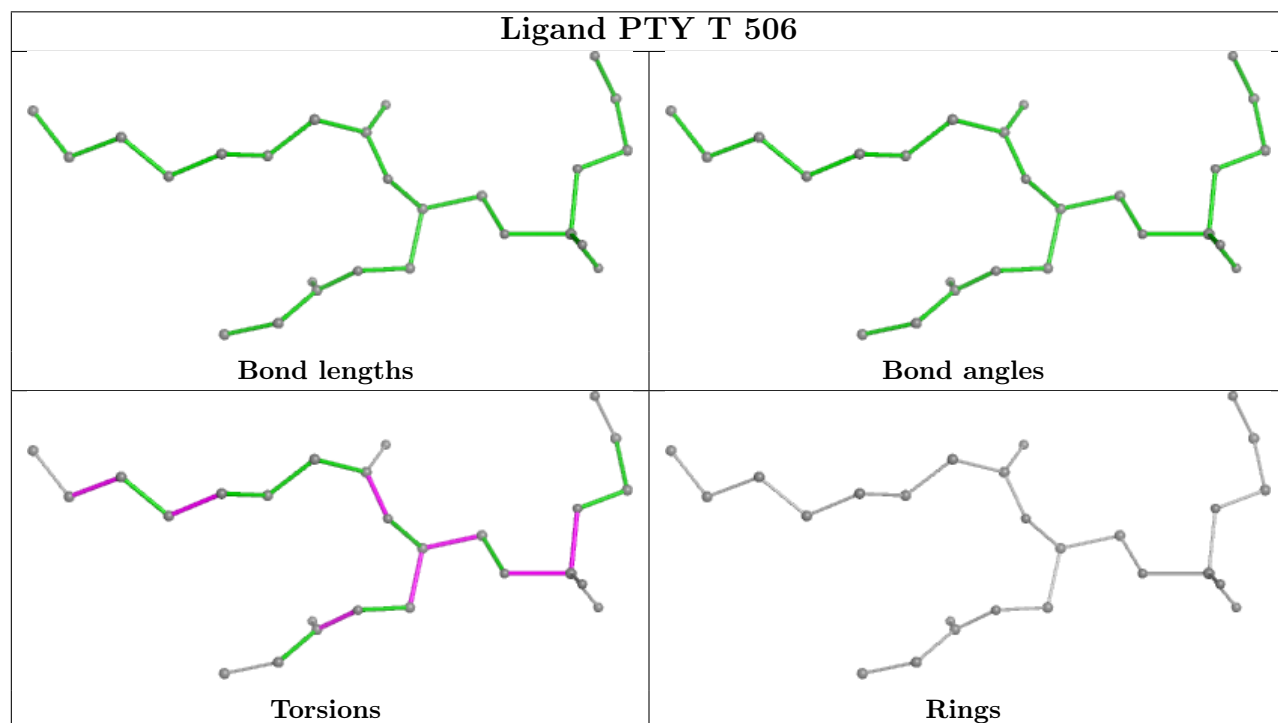
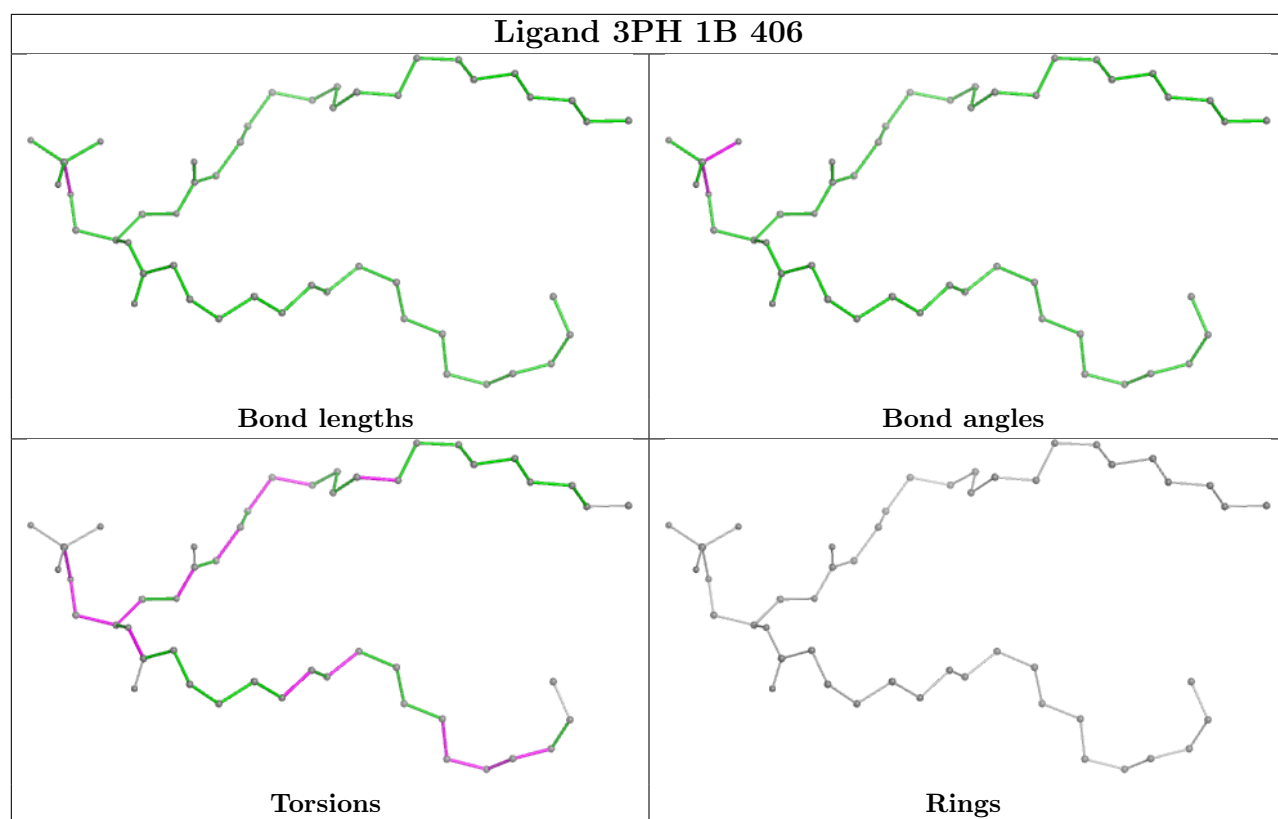
Bond angles

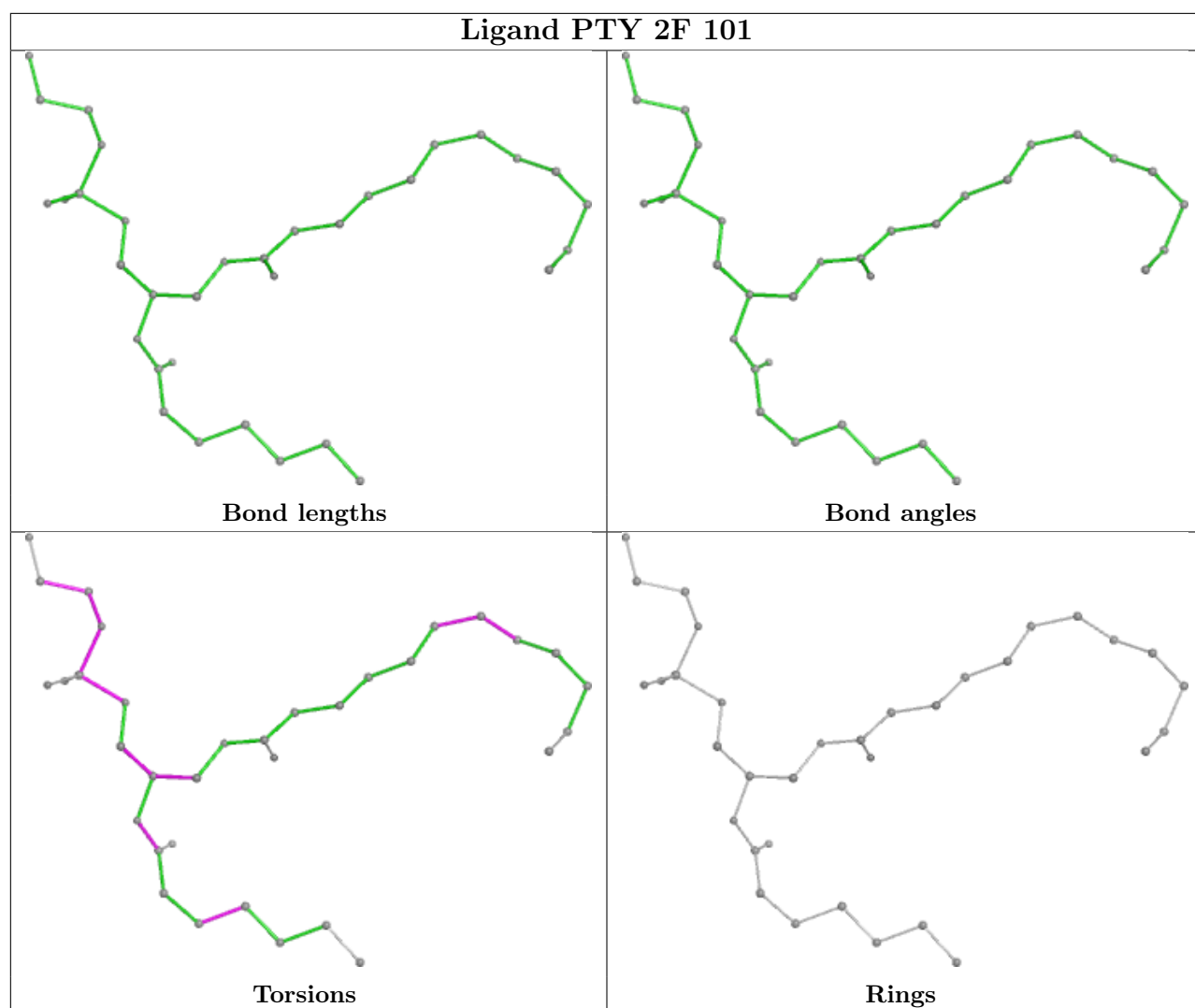


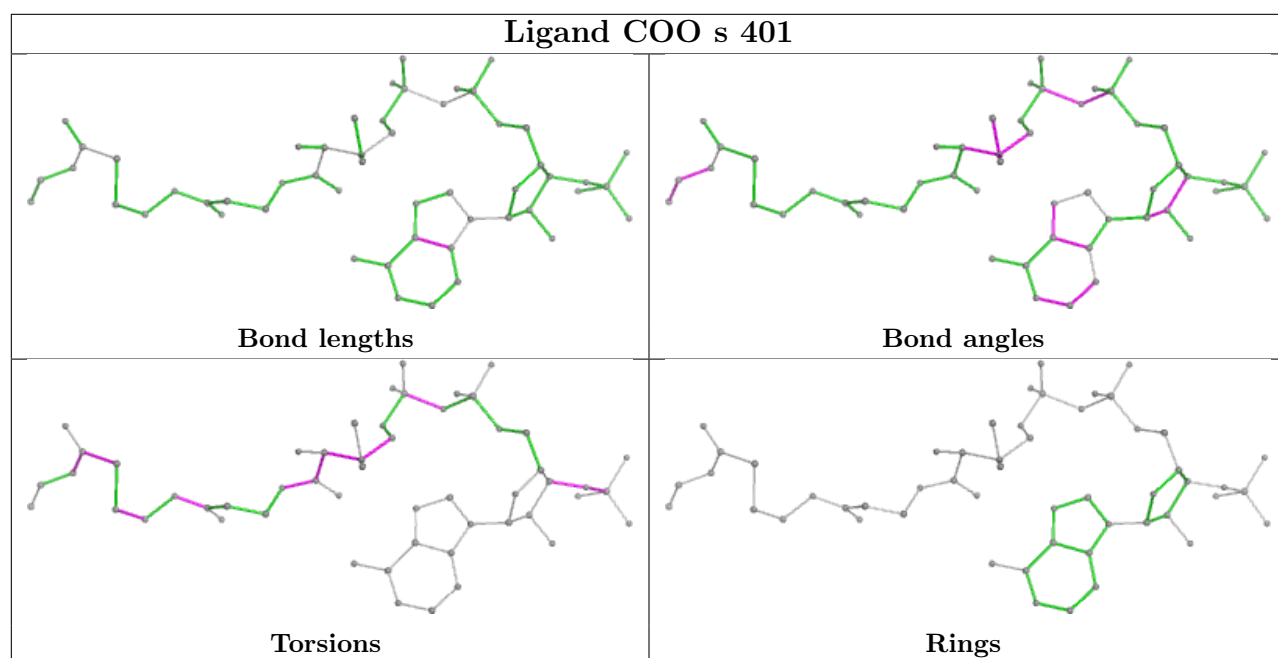
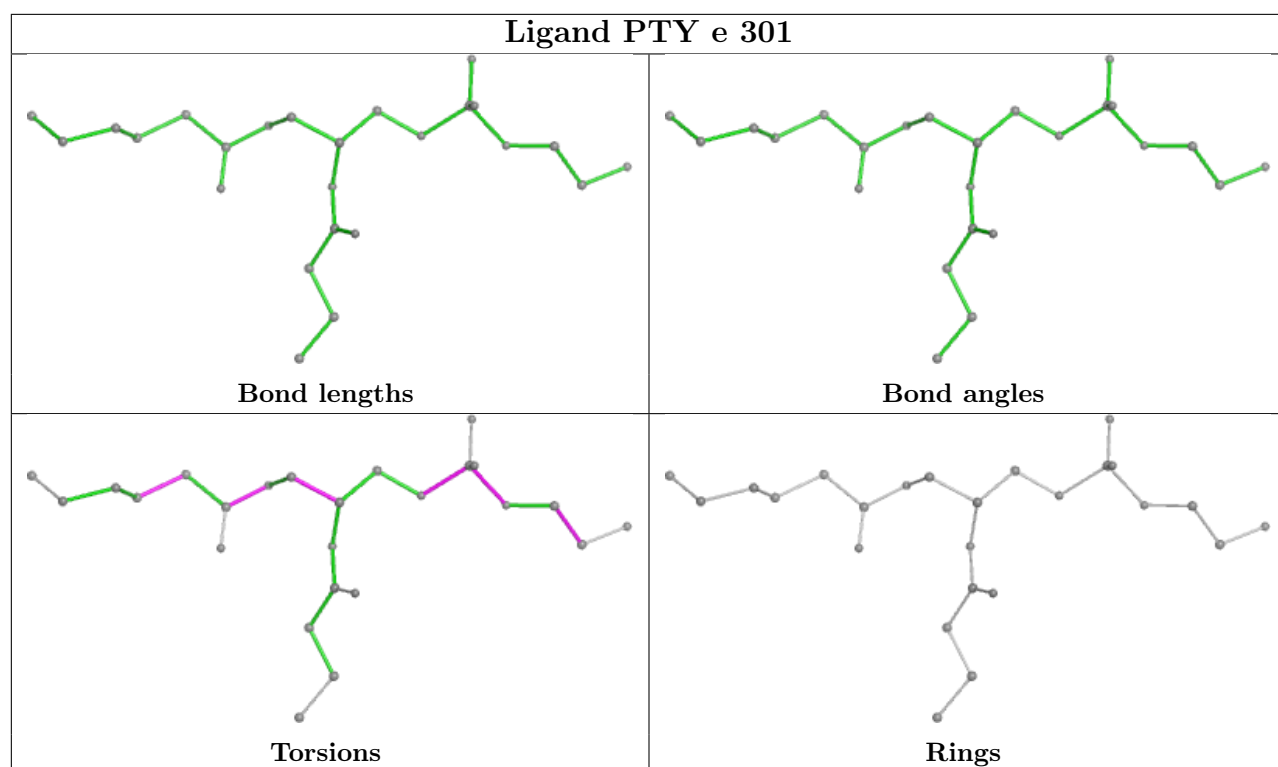
Torsions

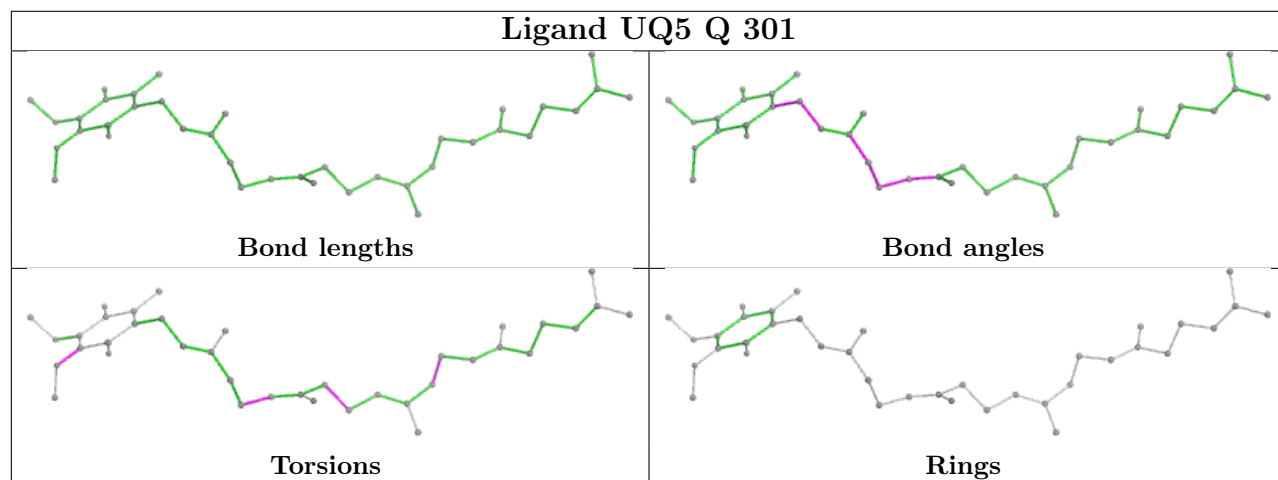
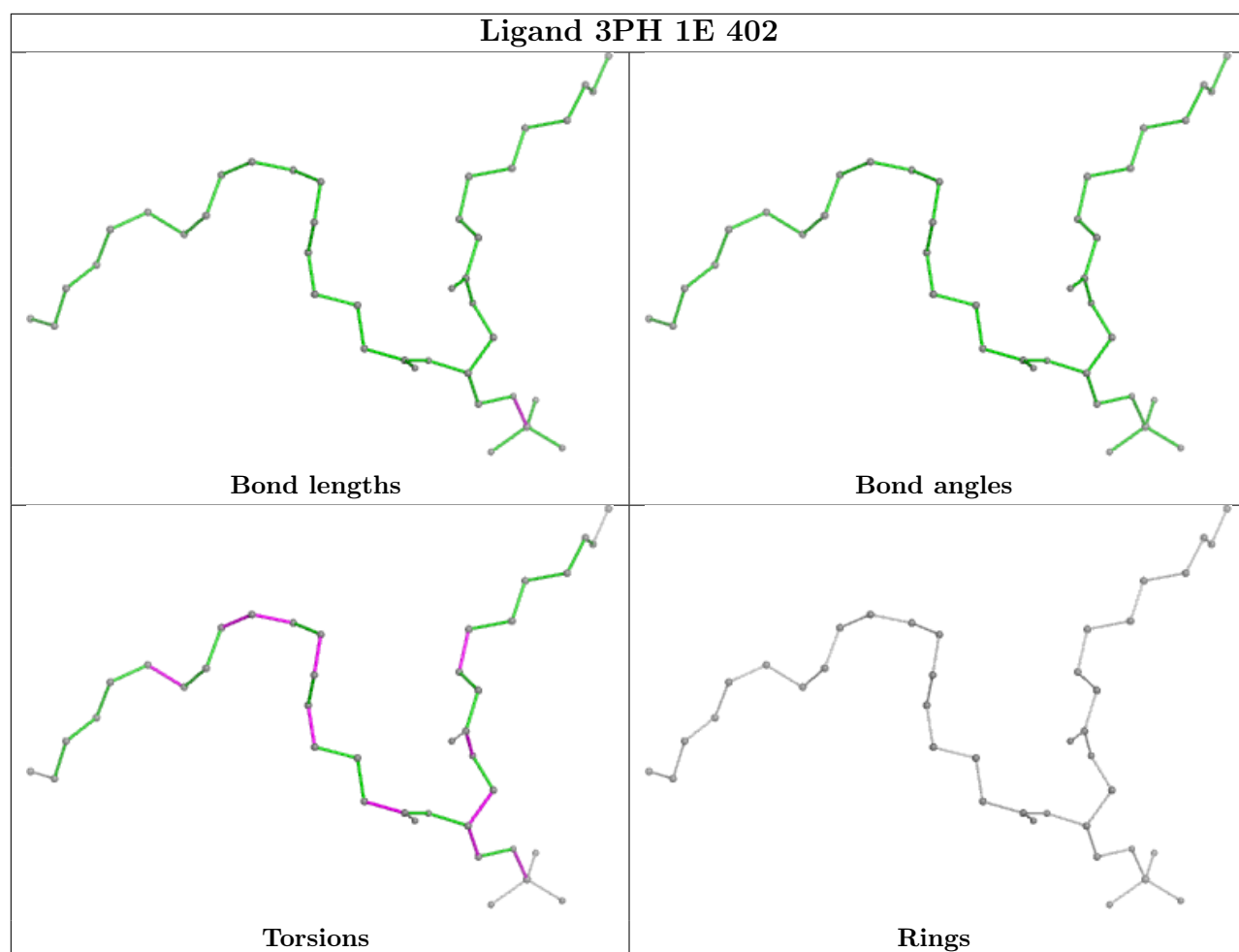


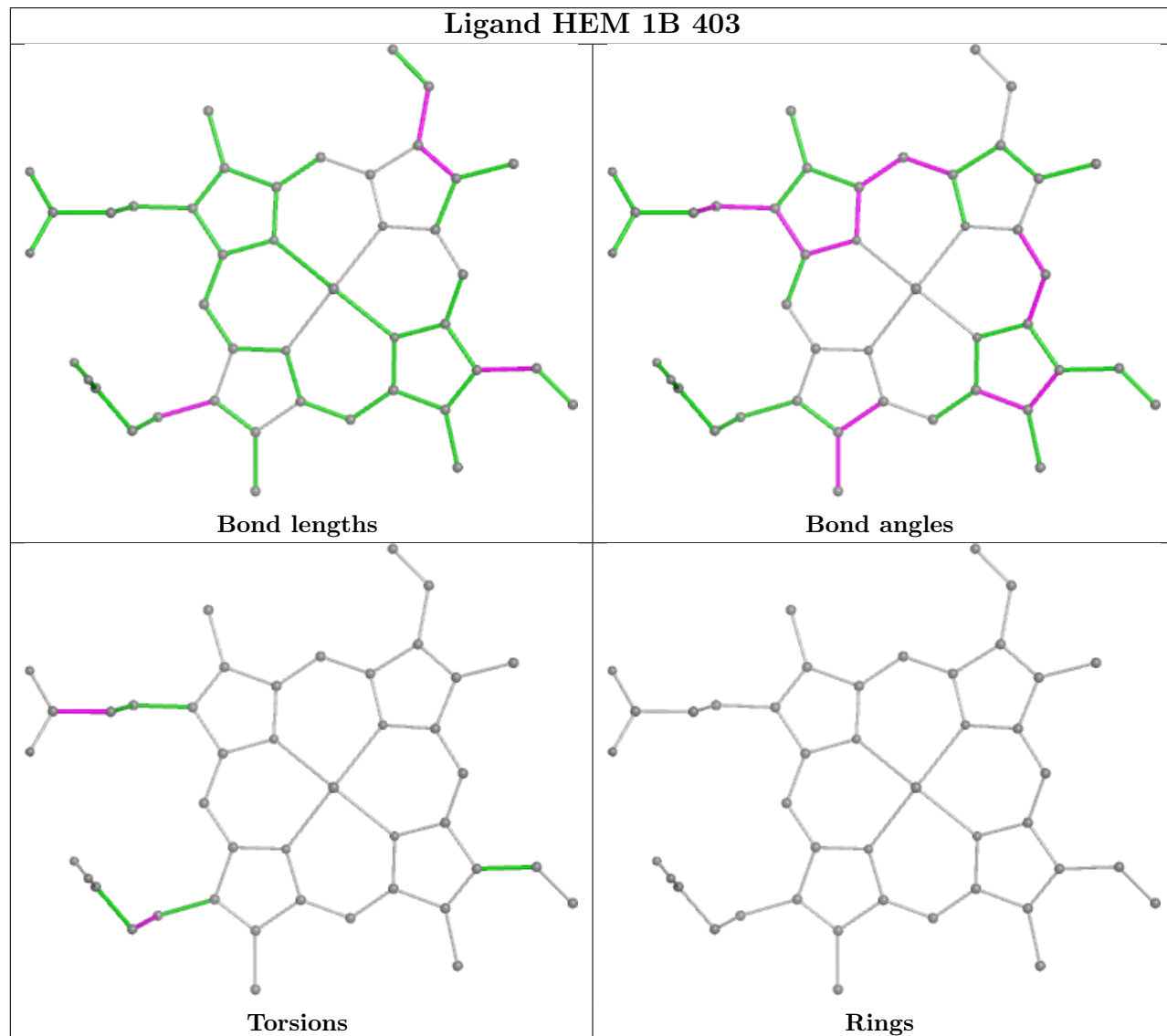
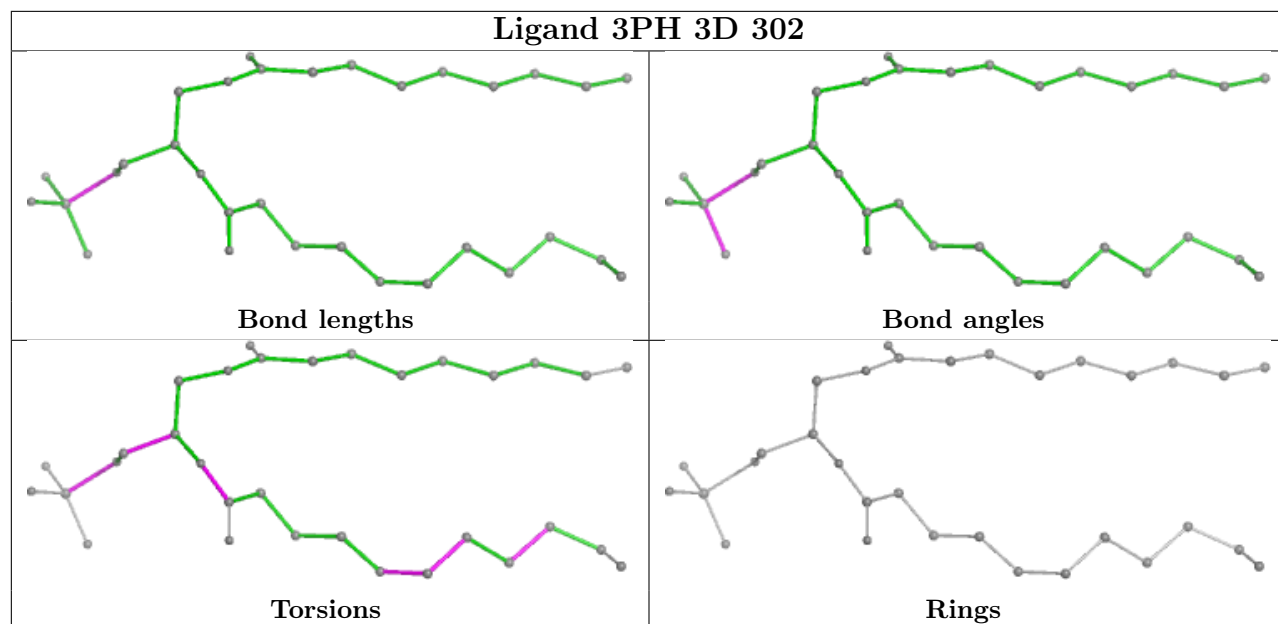
Rings

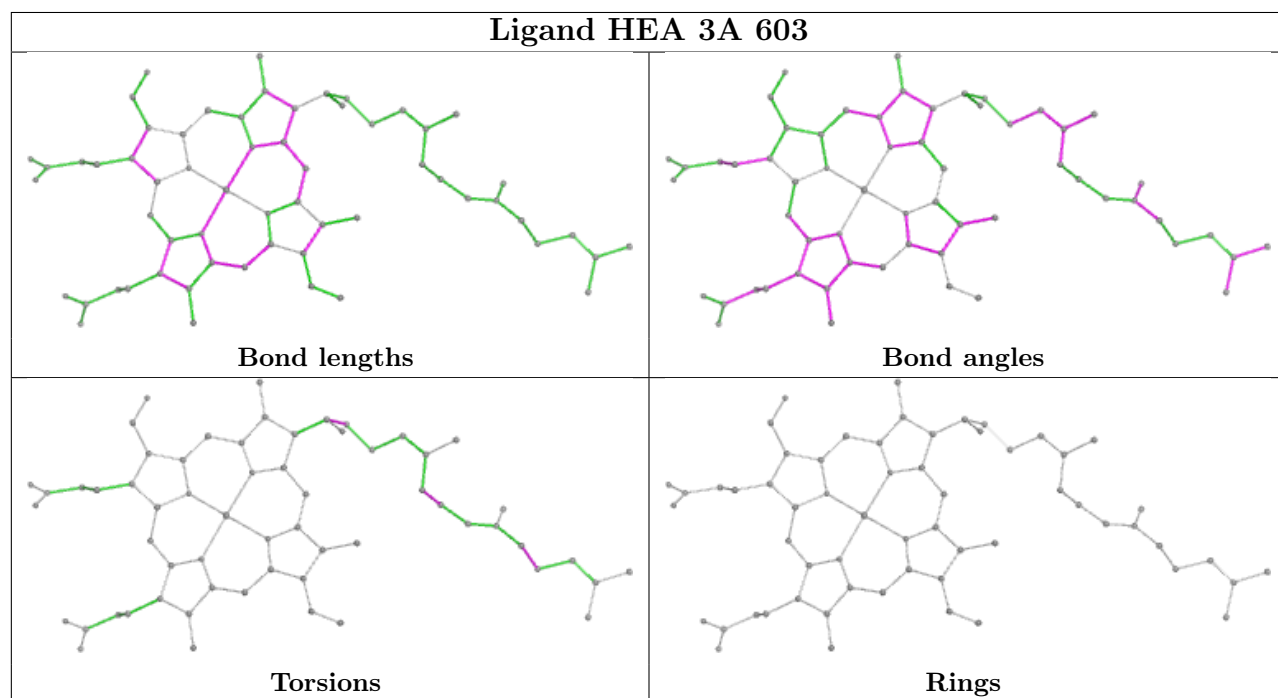
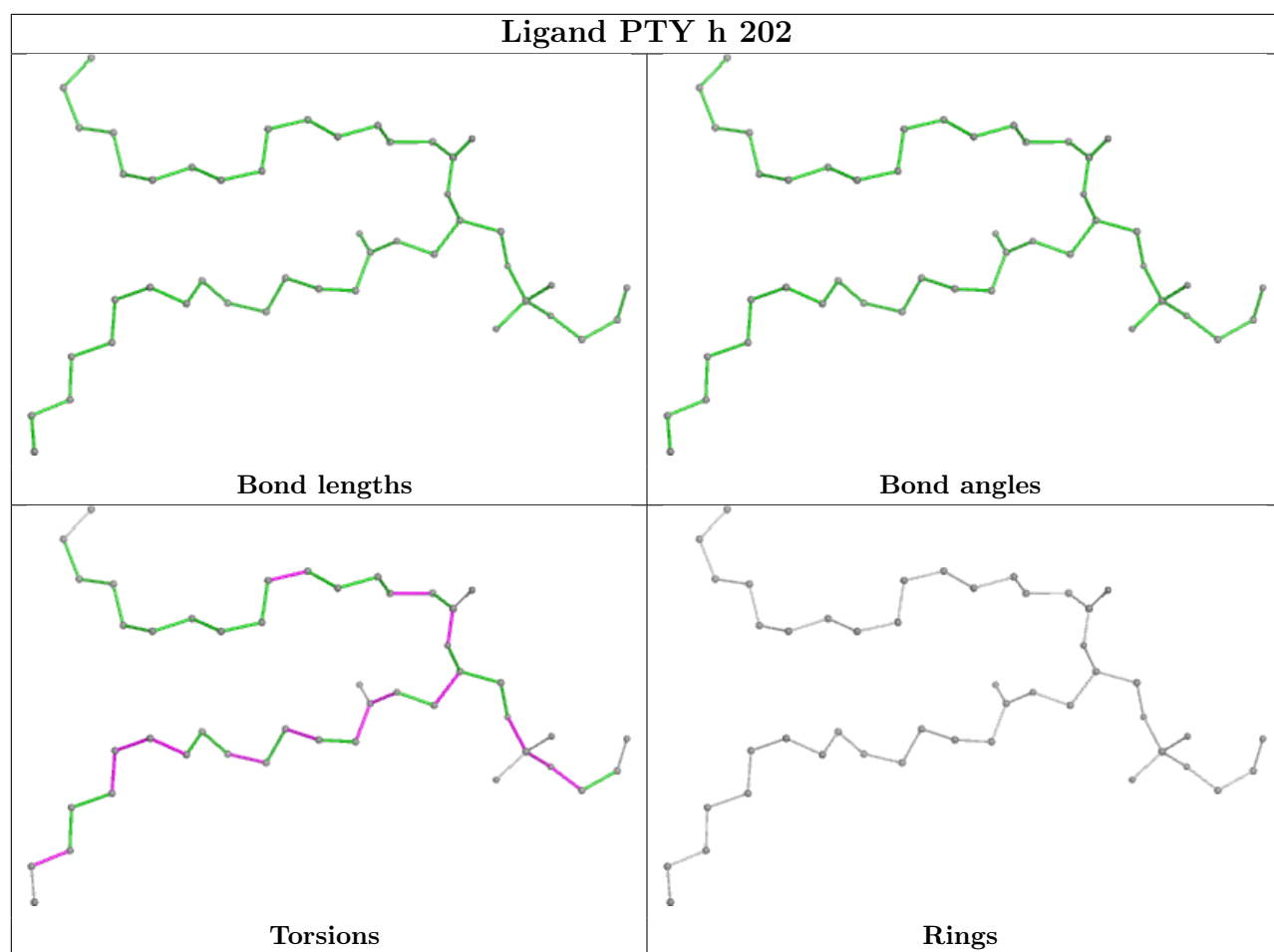


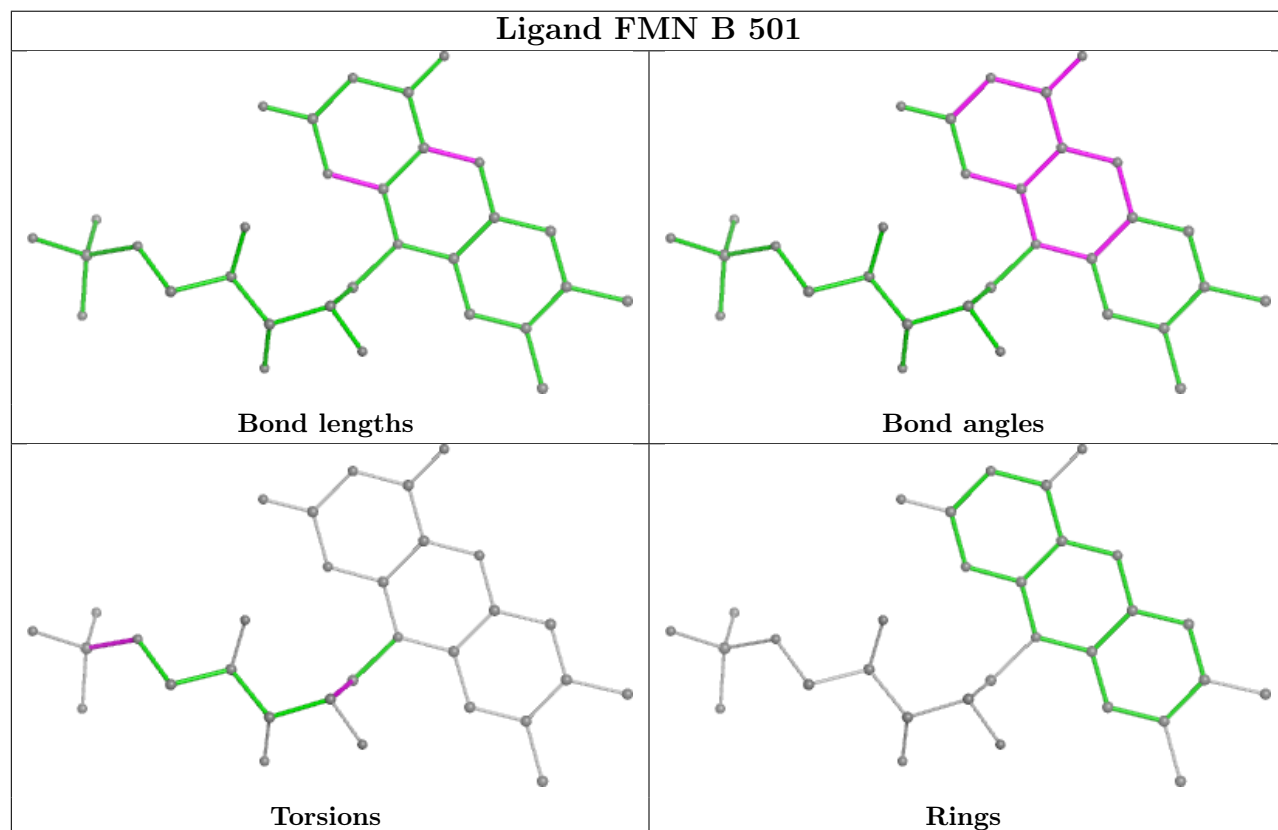
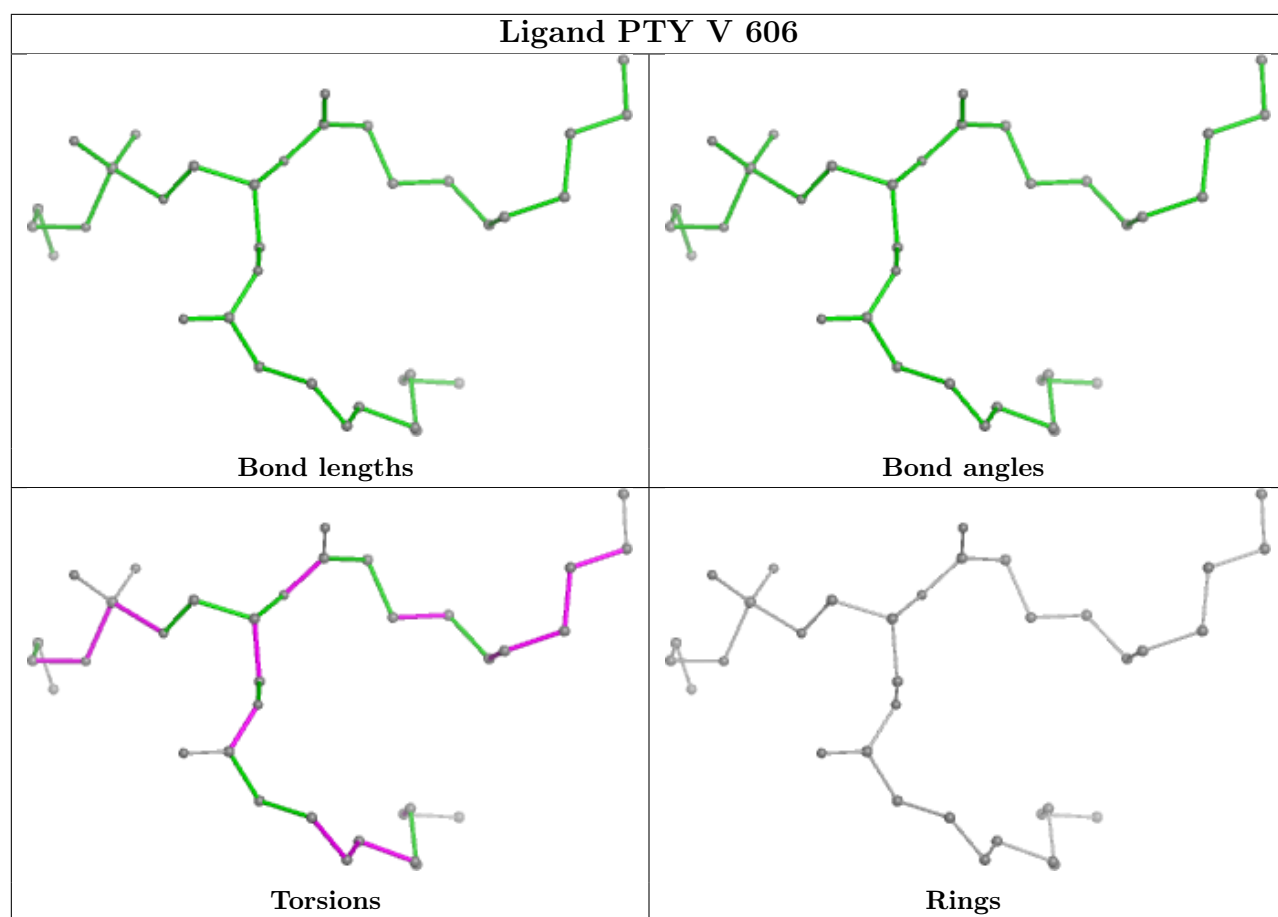


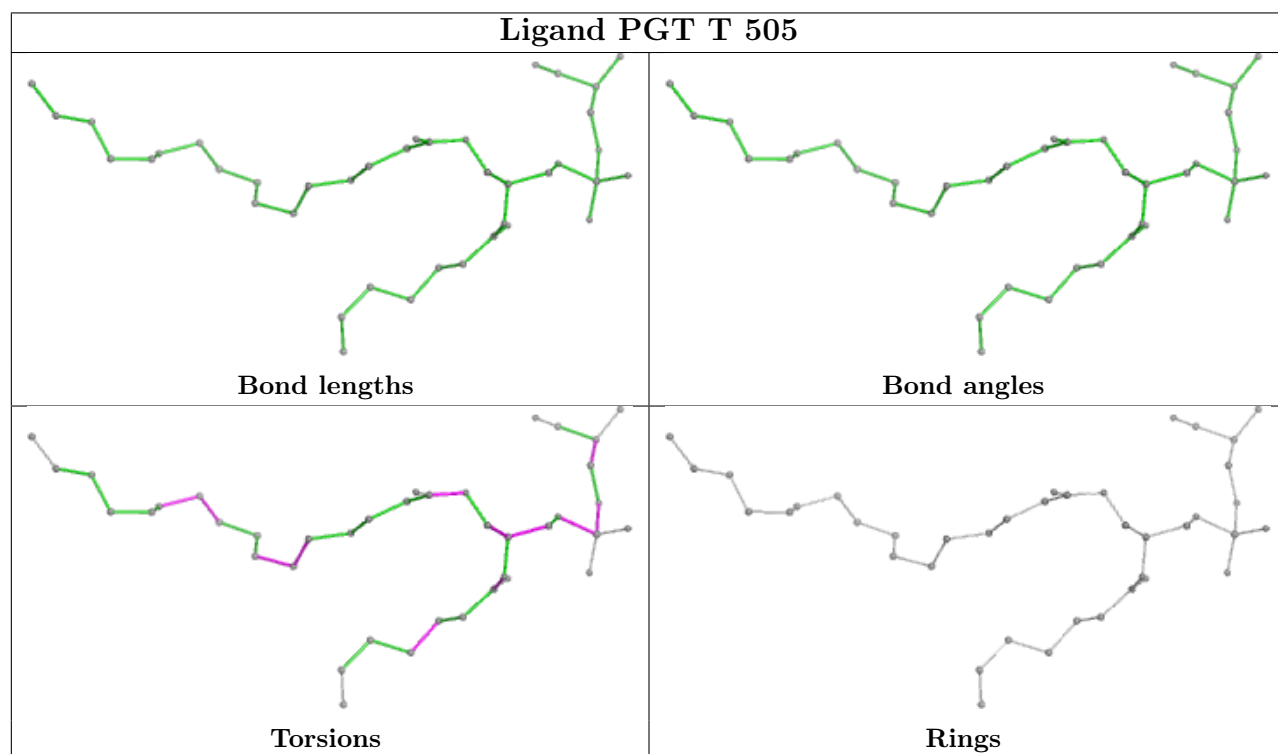
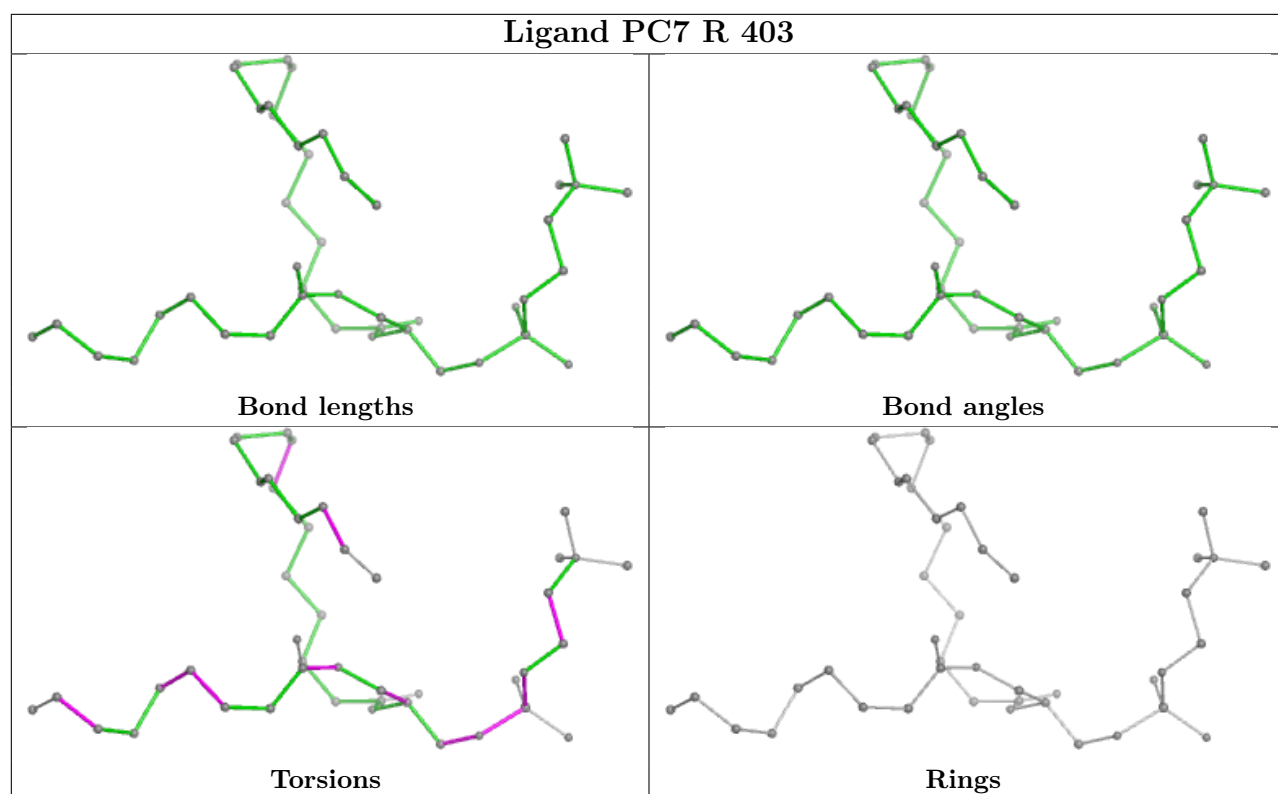


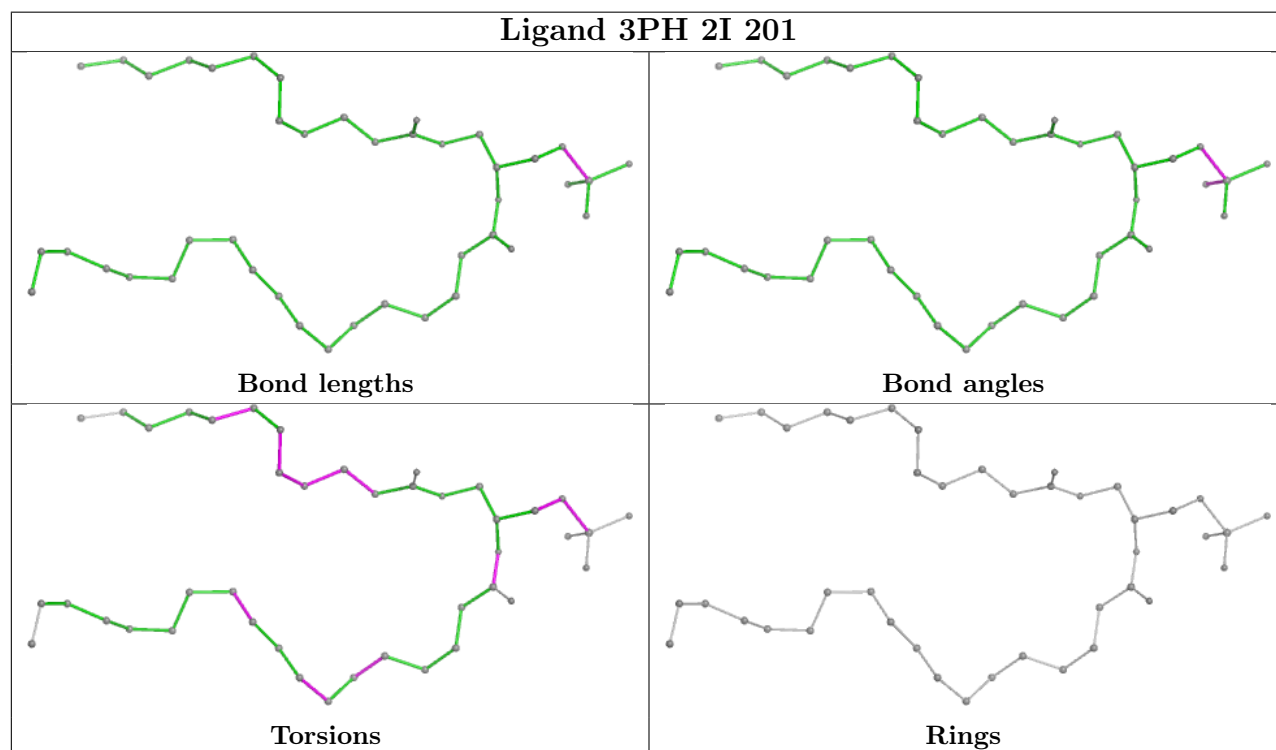
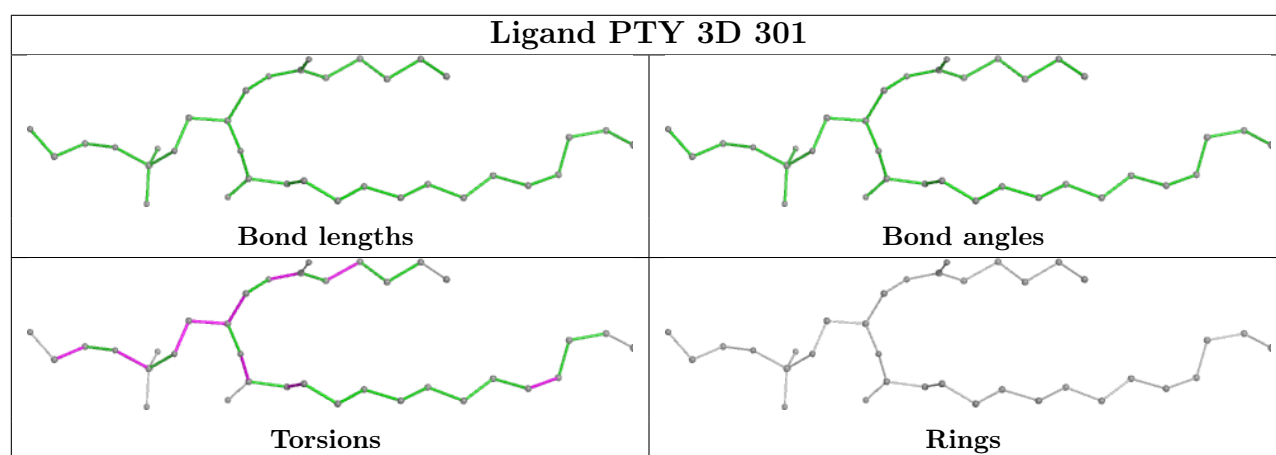
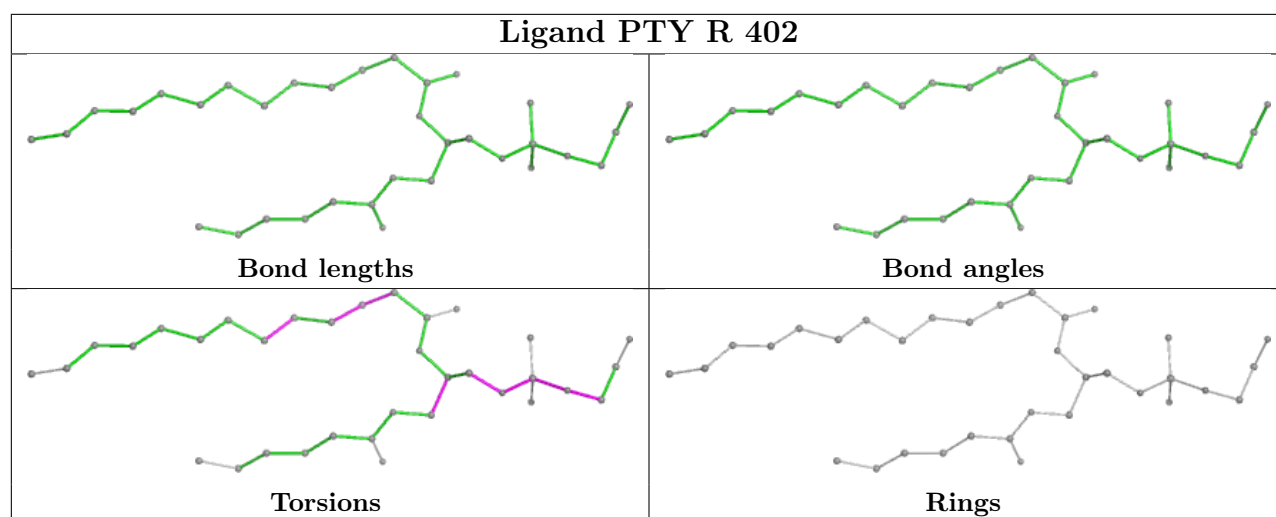


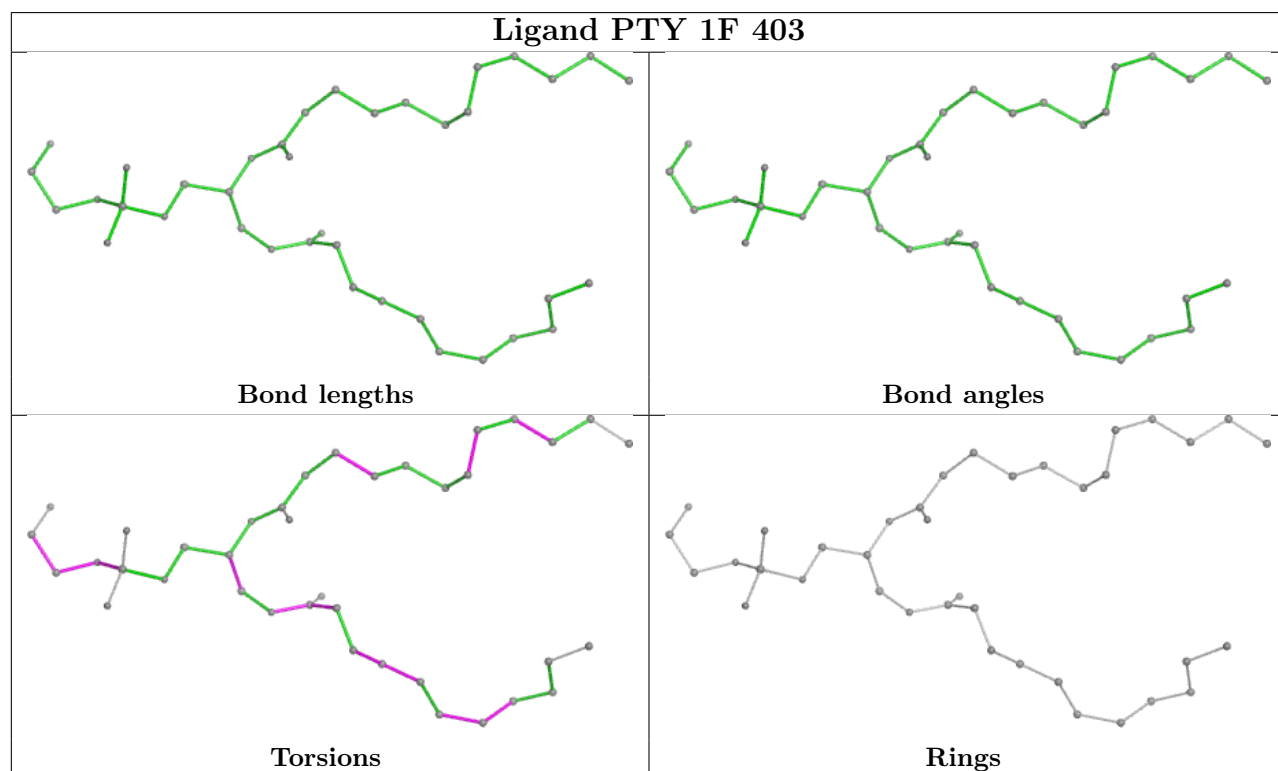
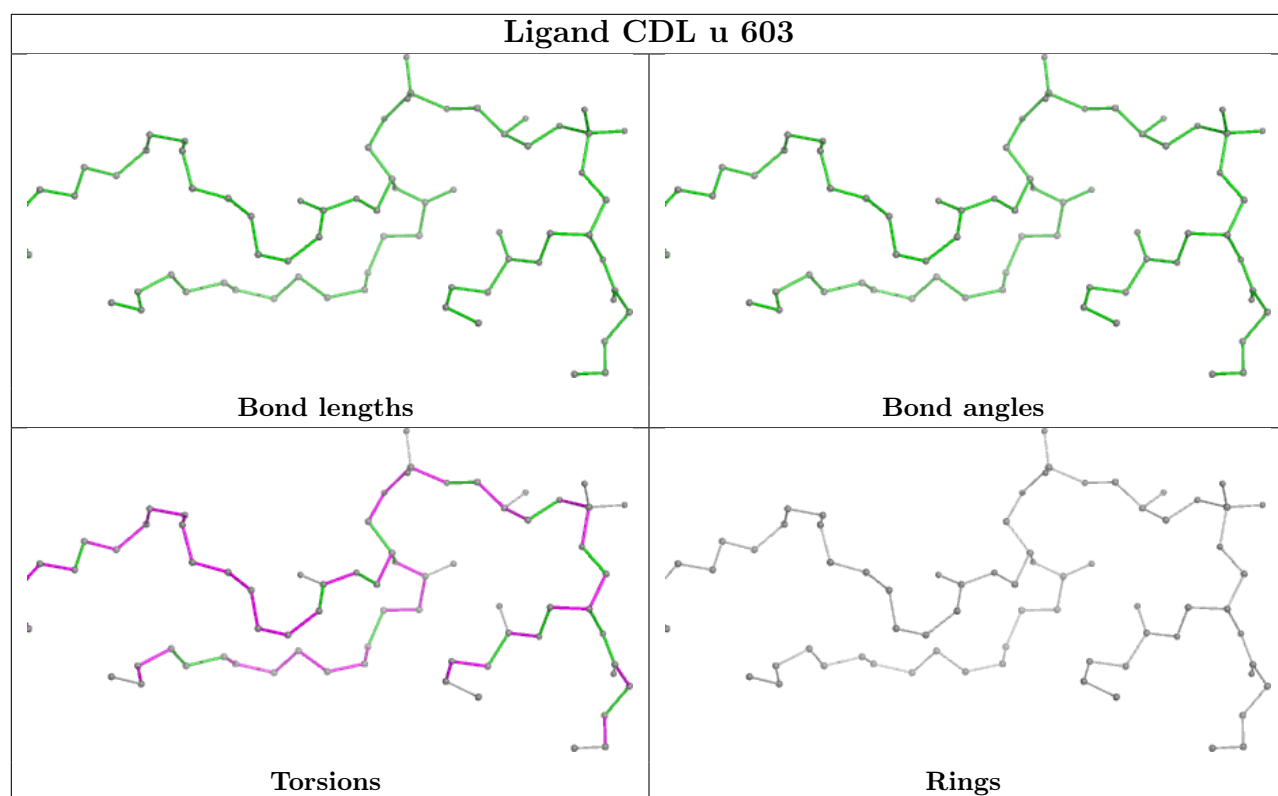


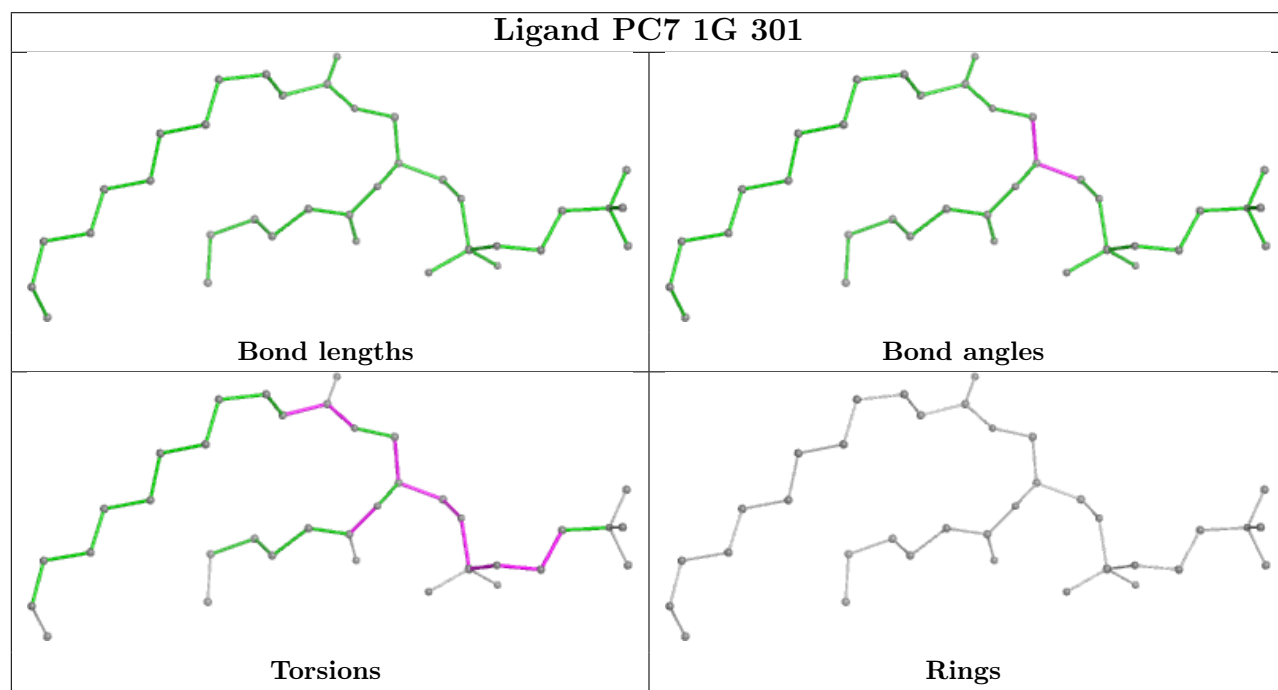
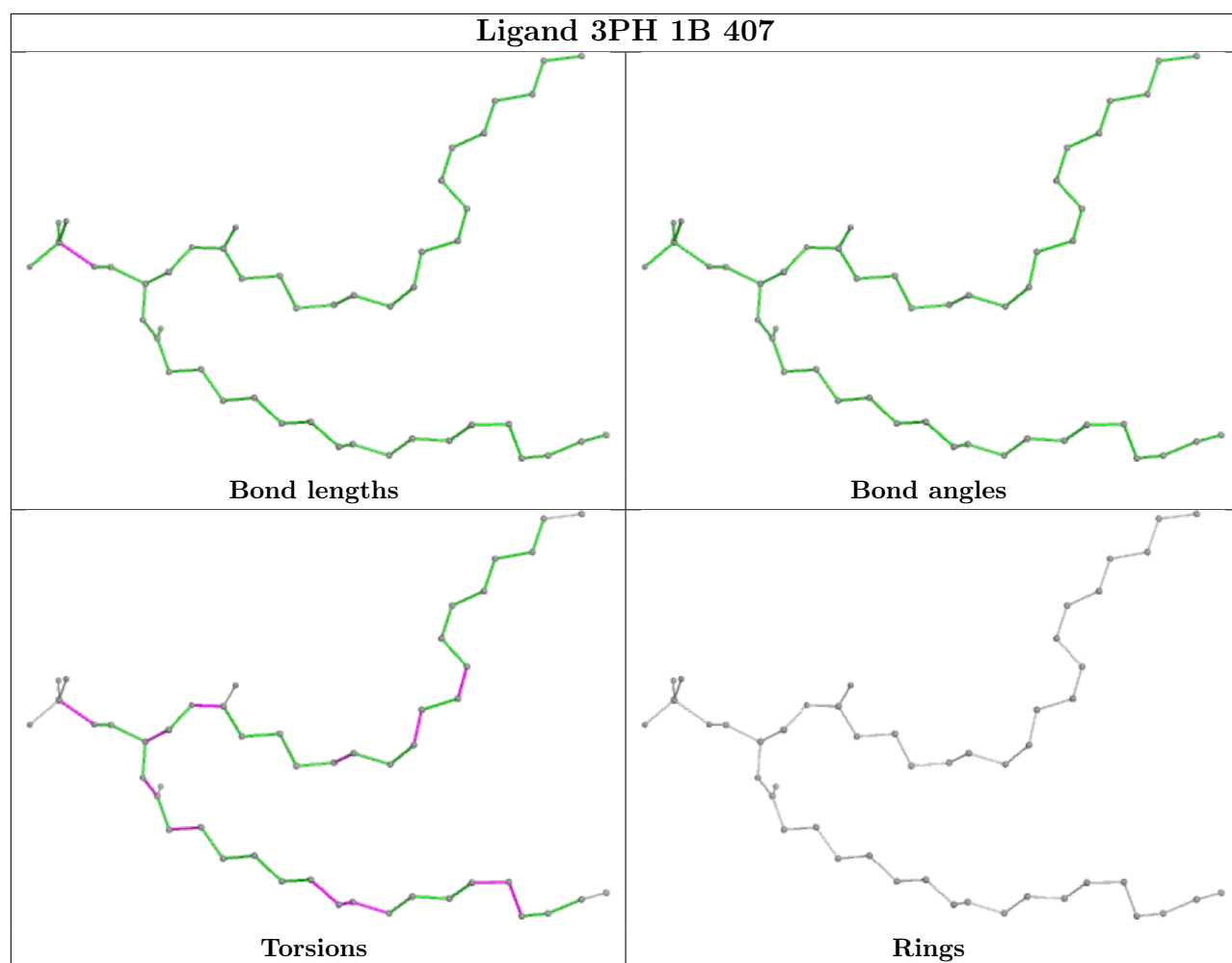


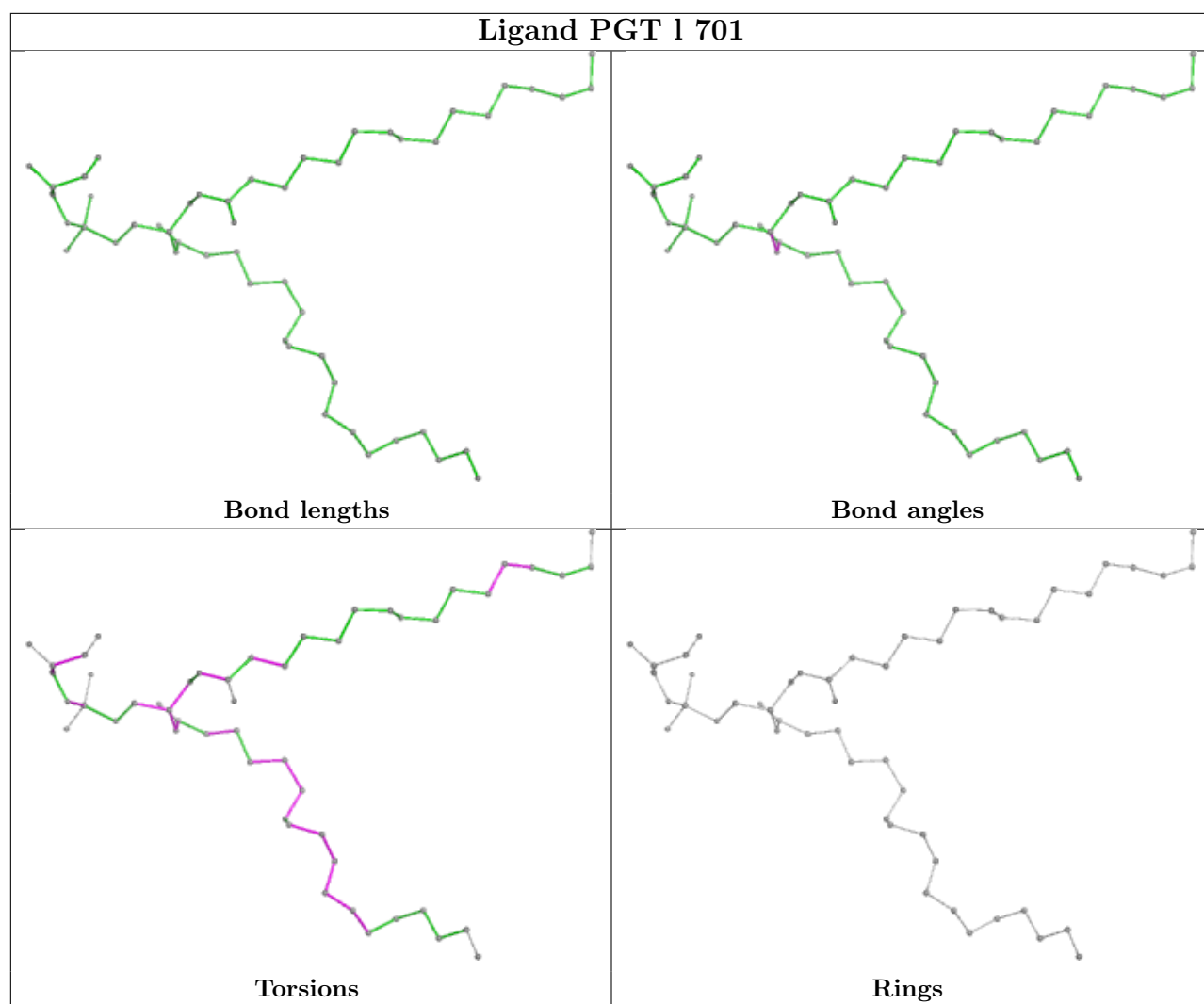


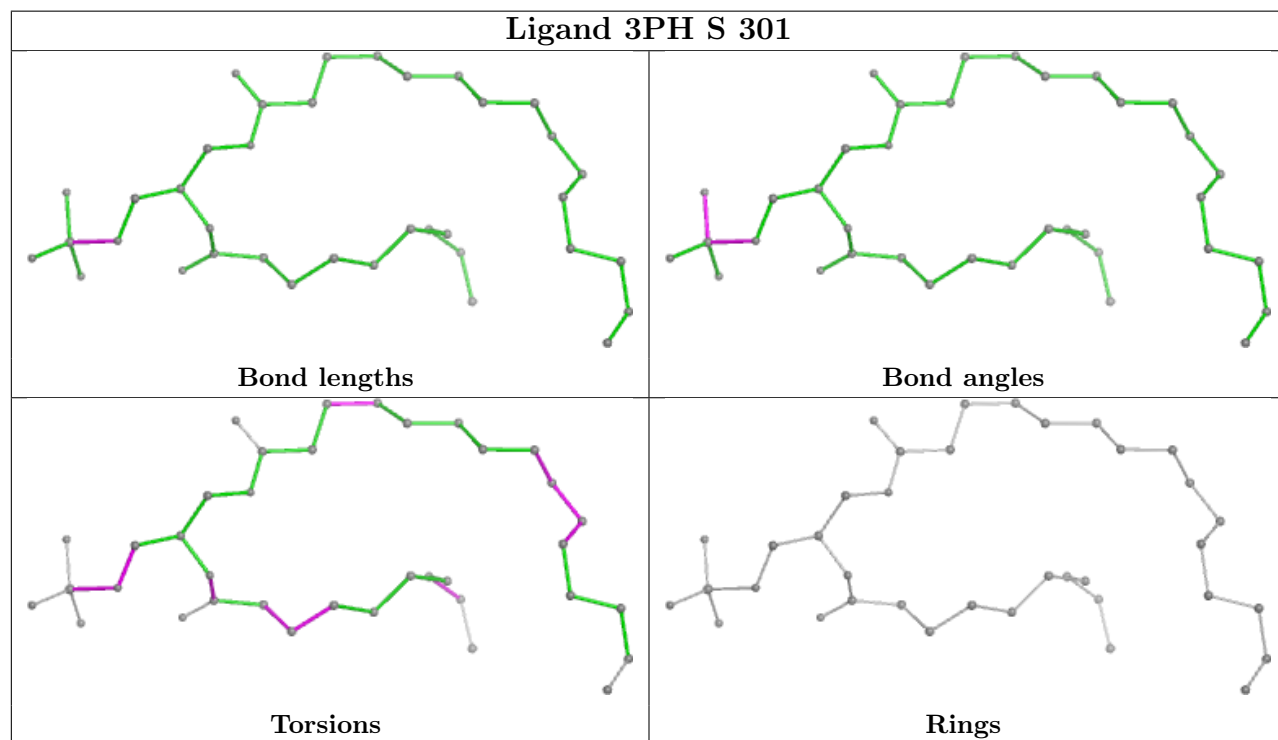
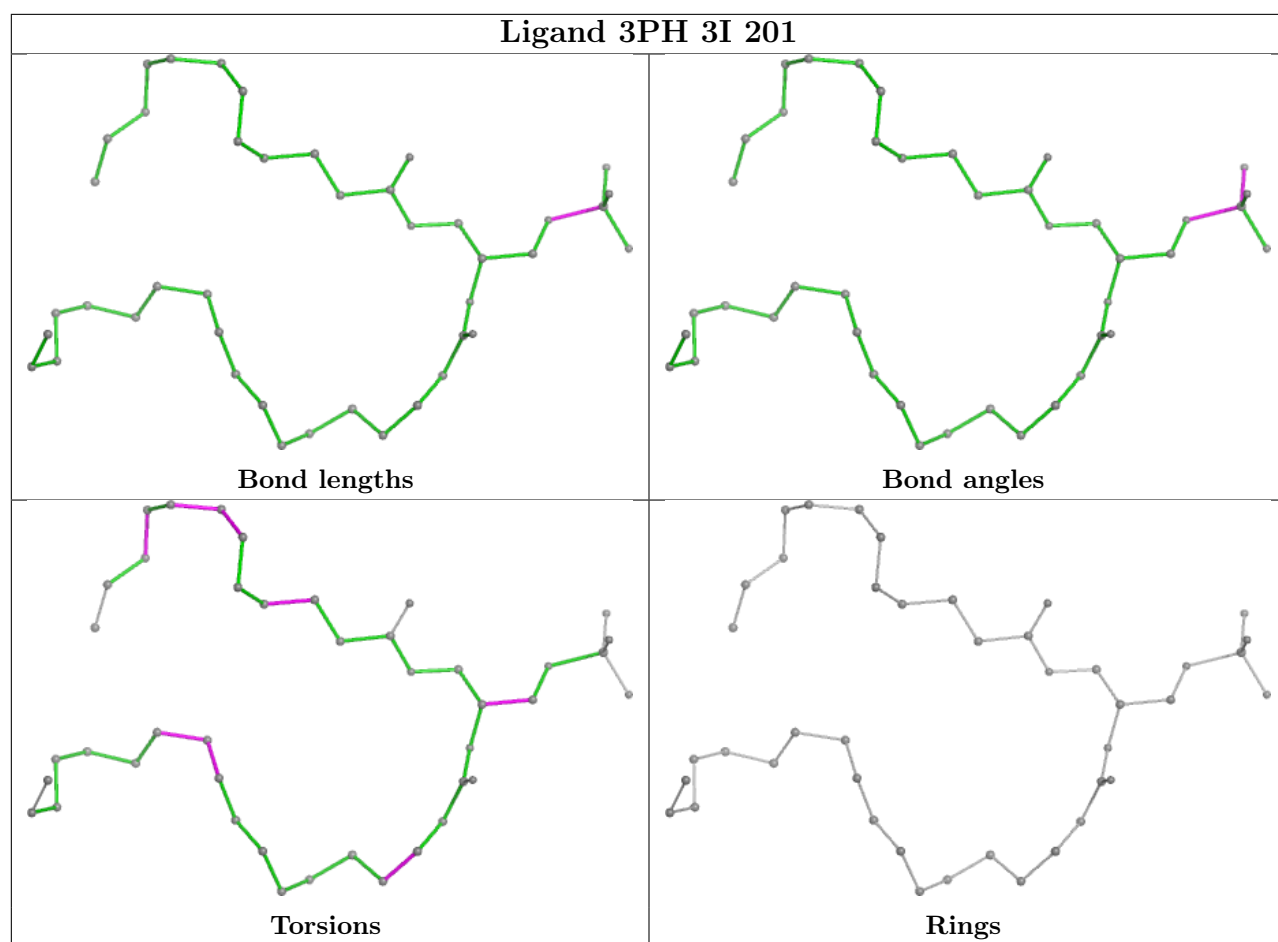


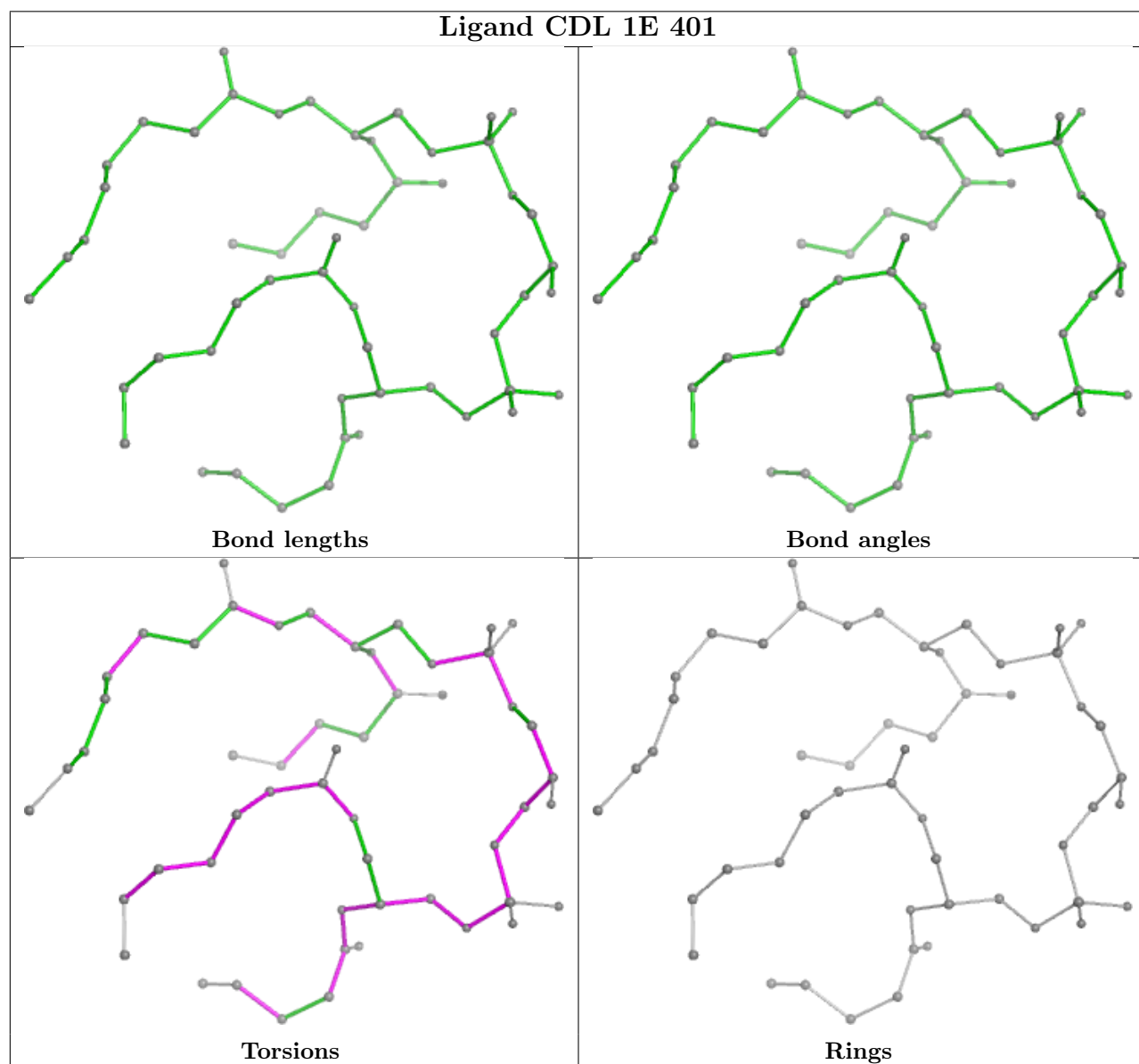
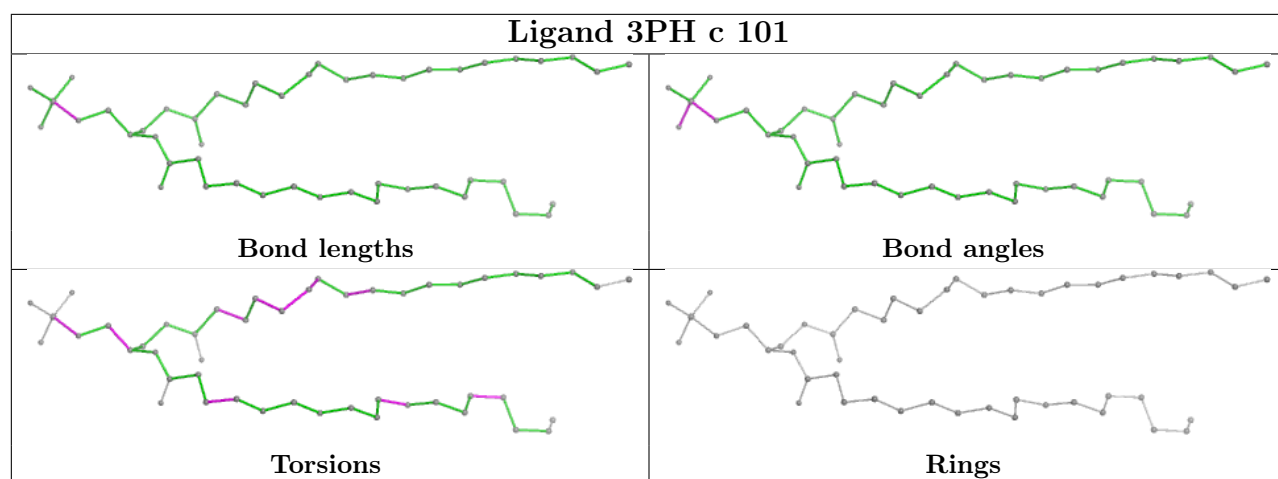


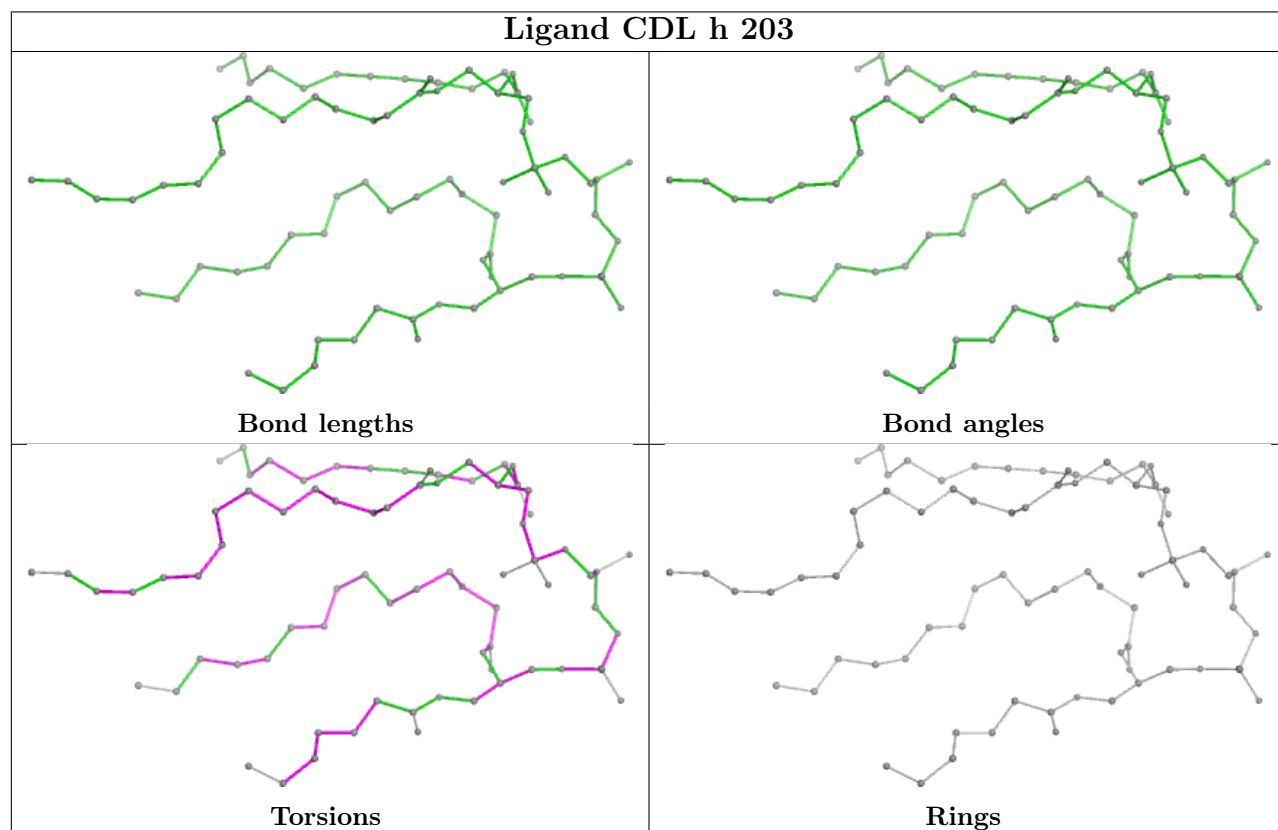
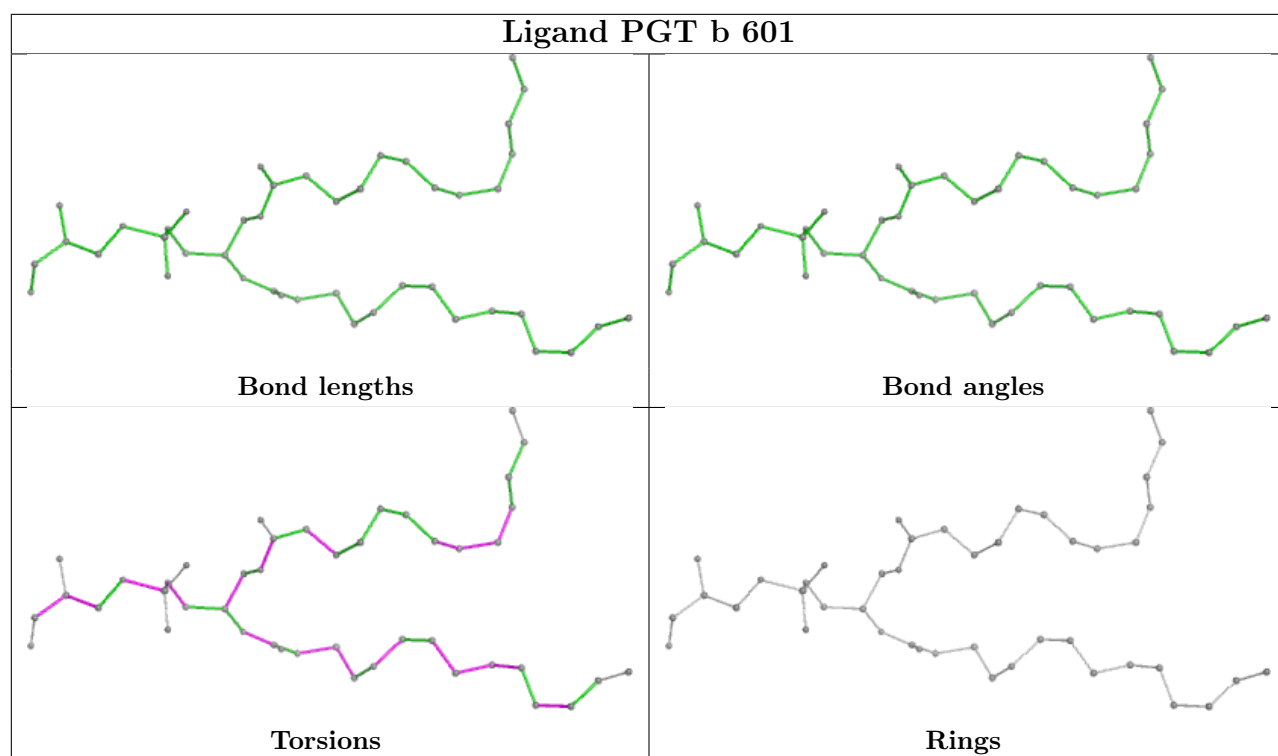


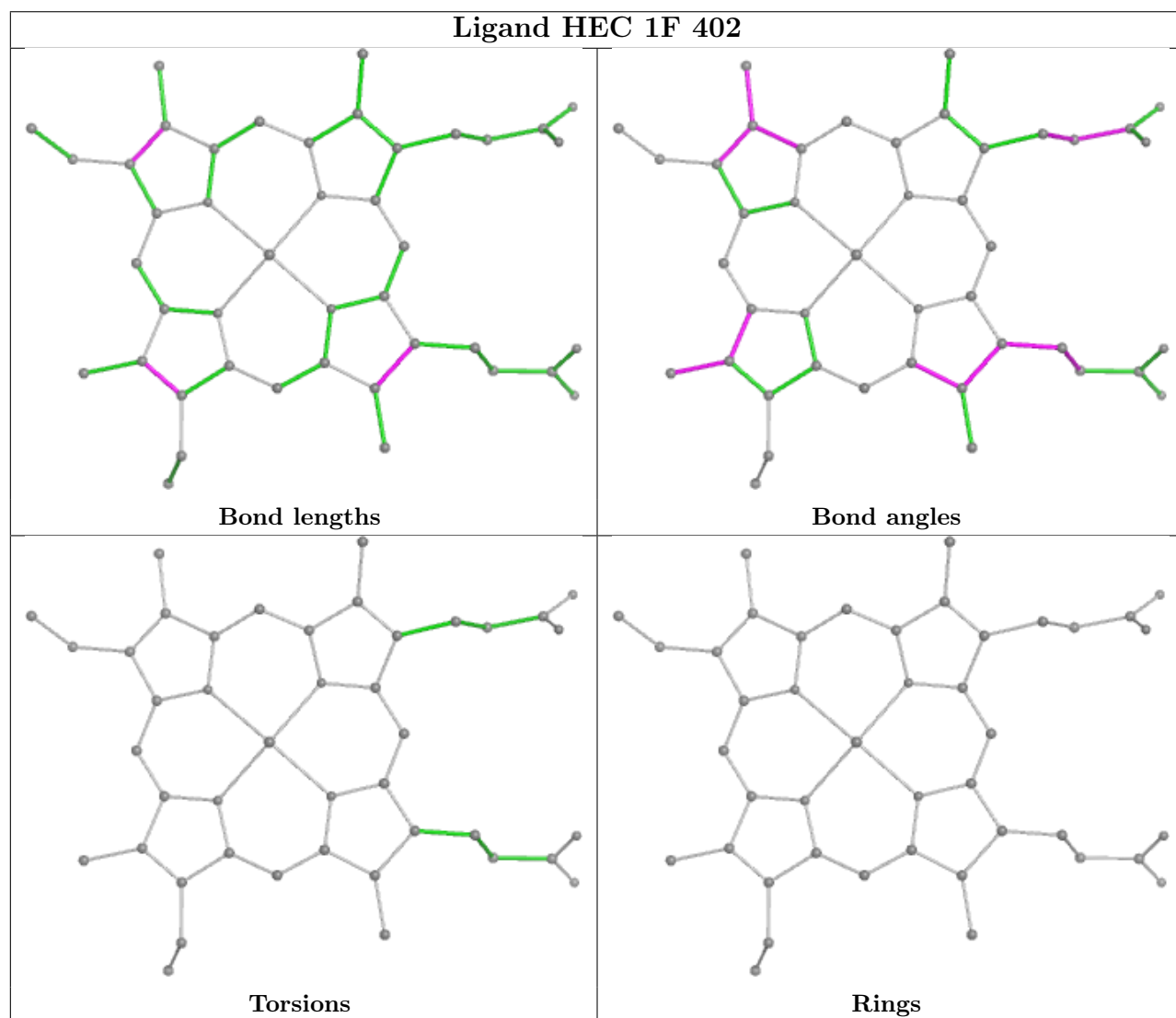
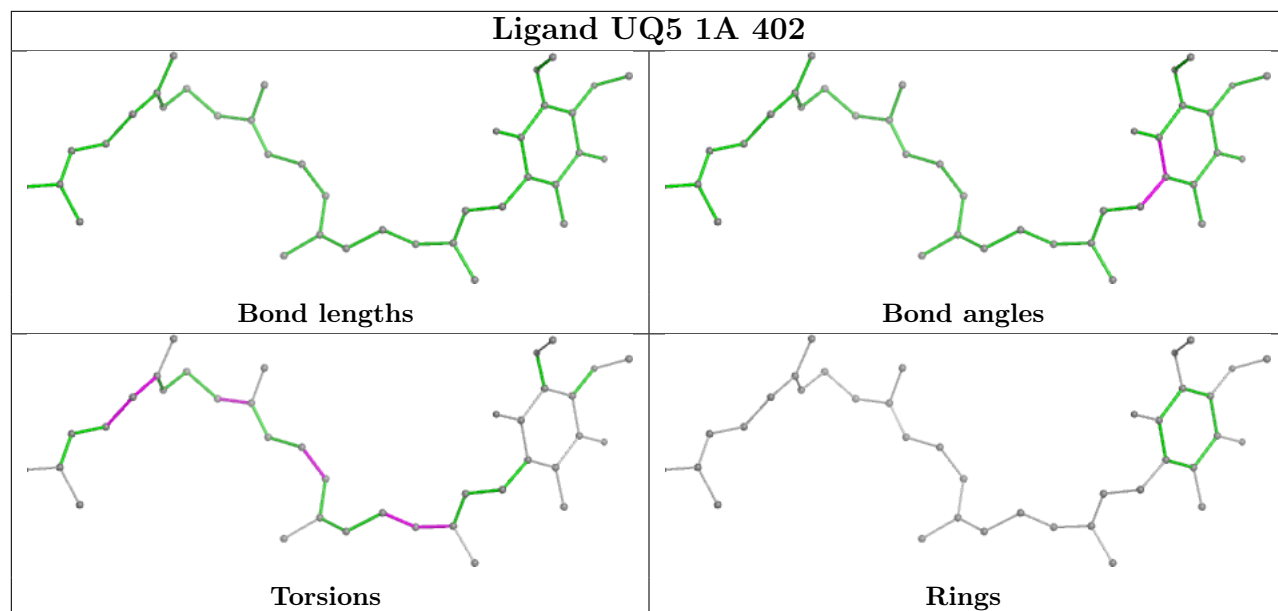


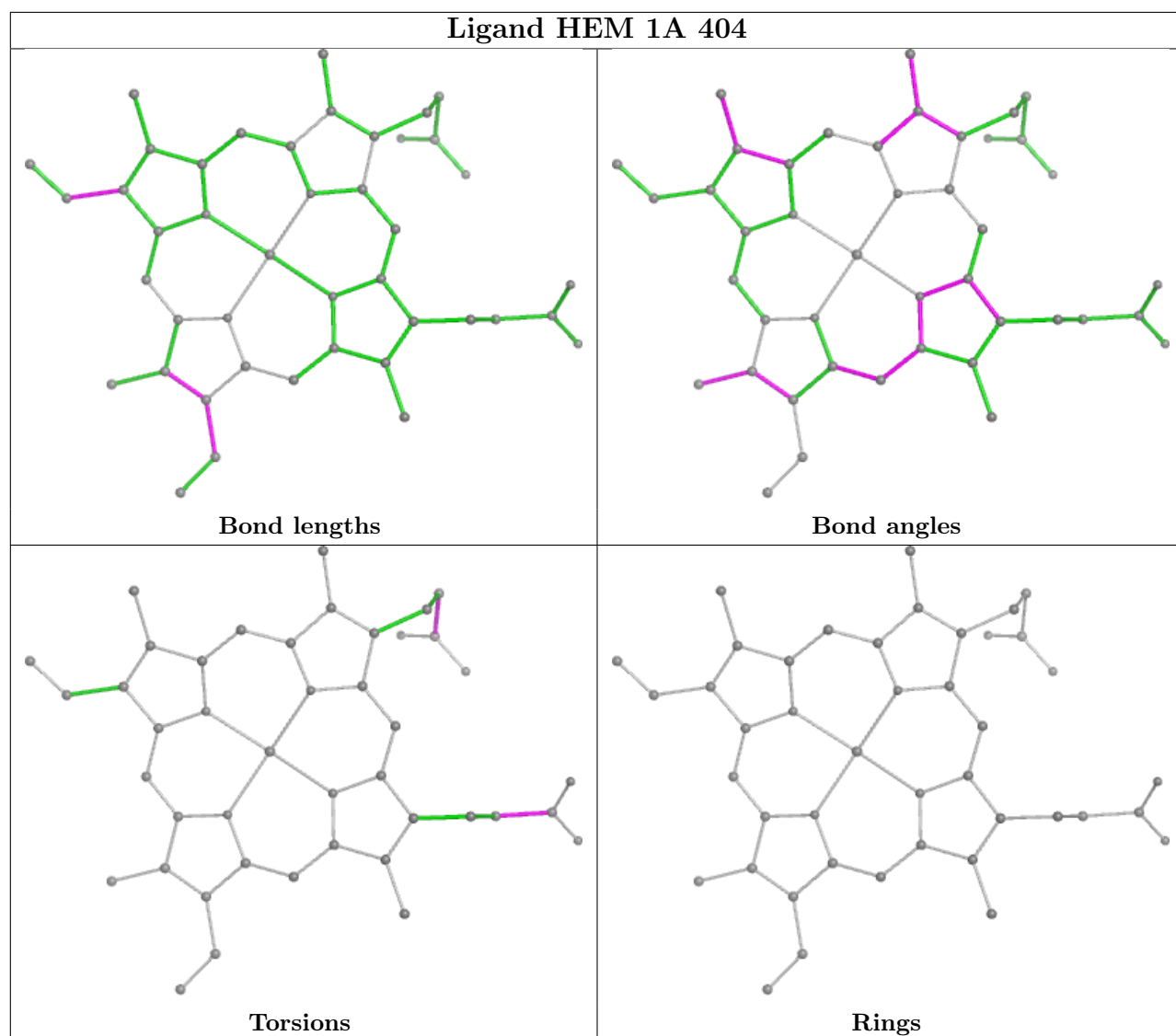
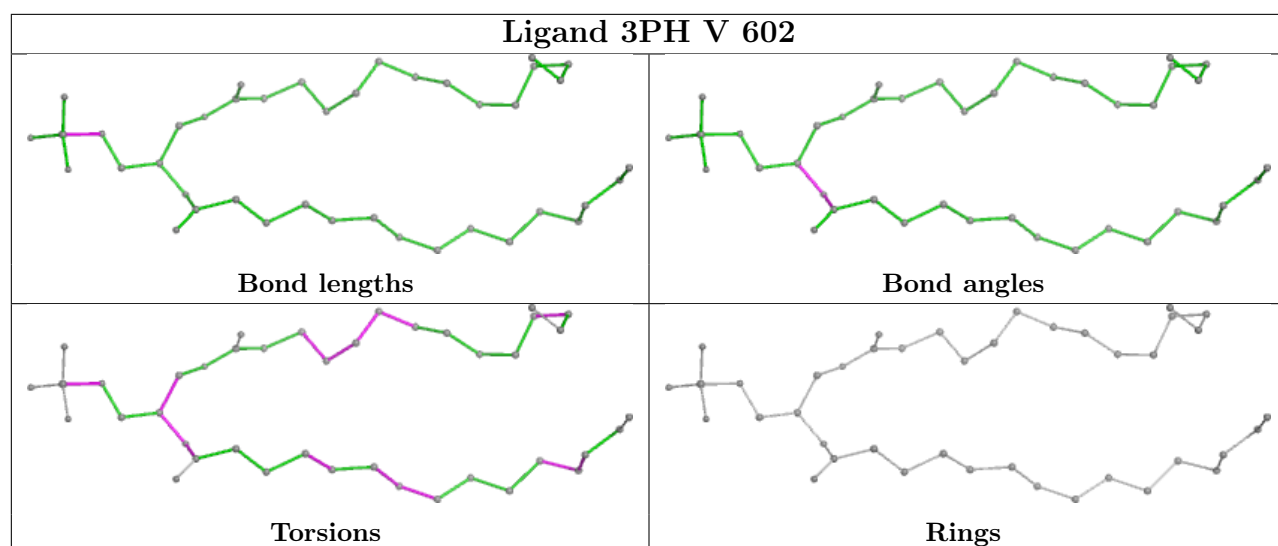


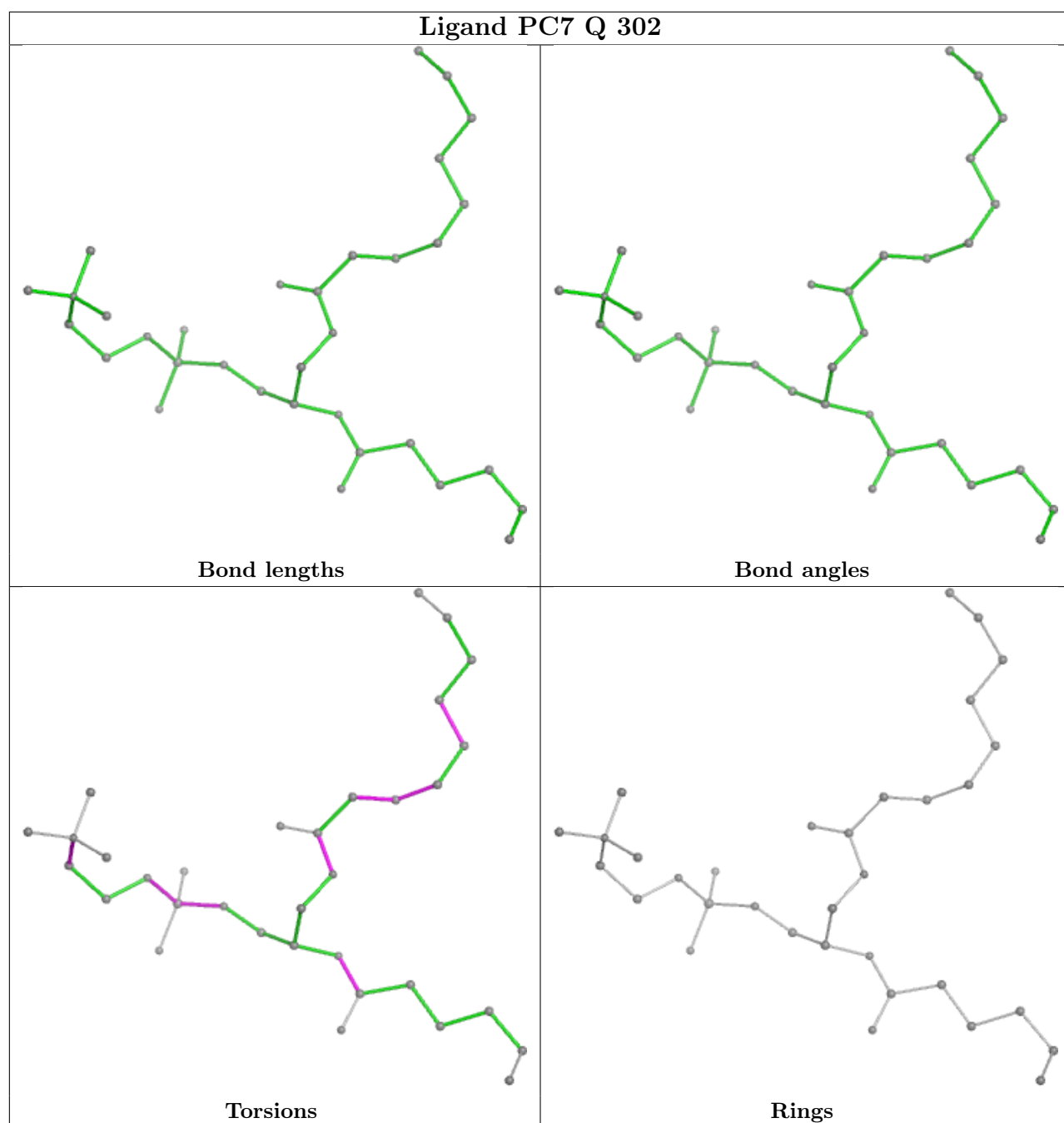


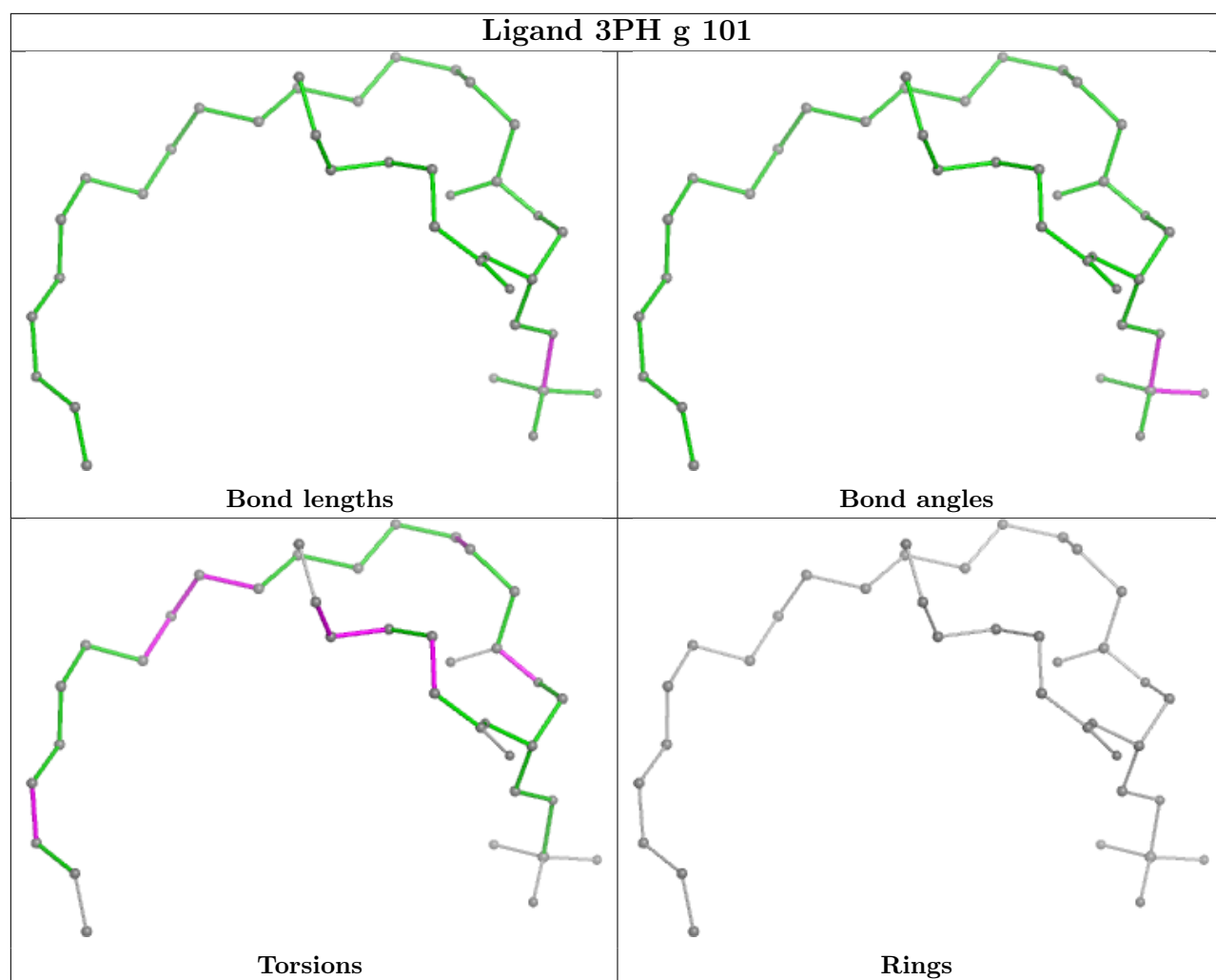


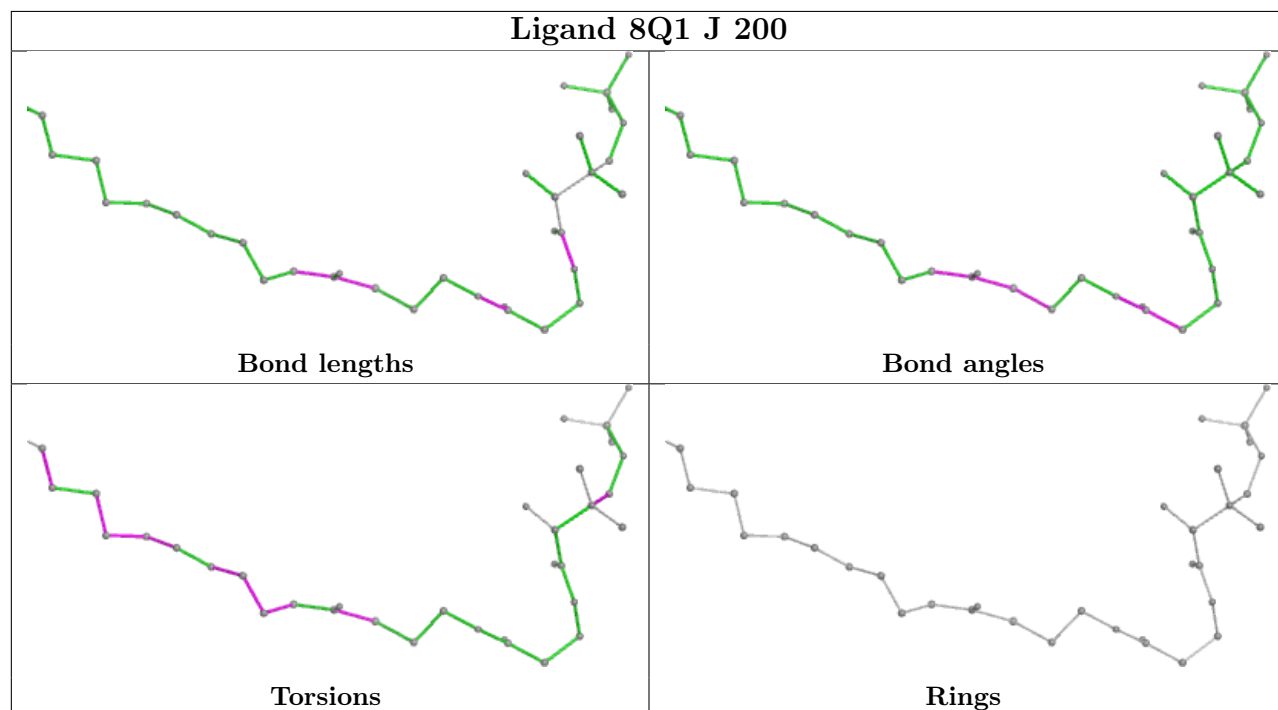
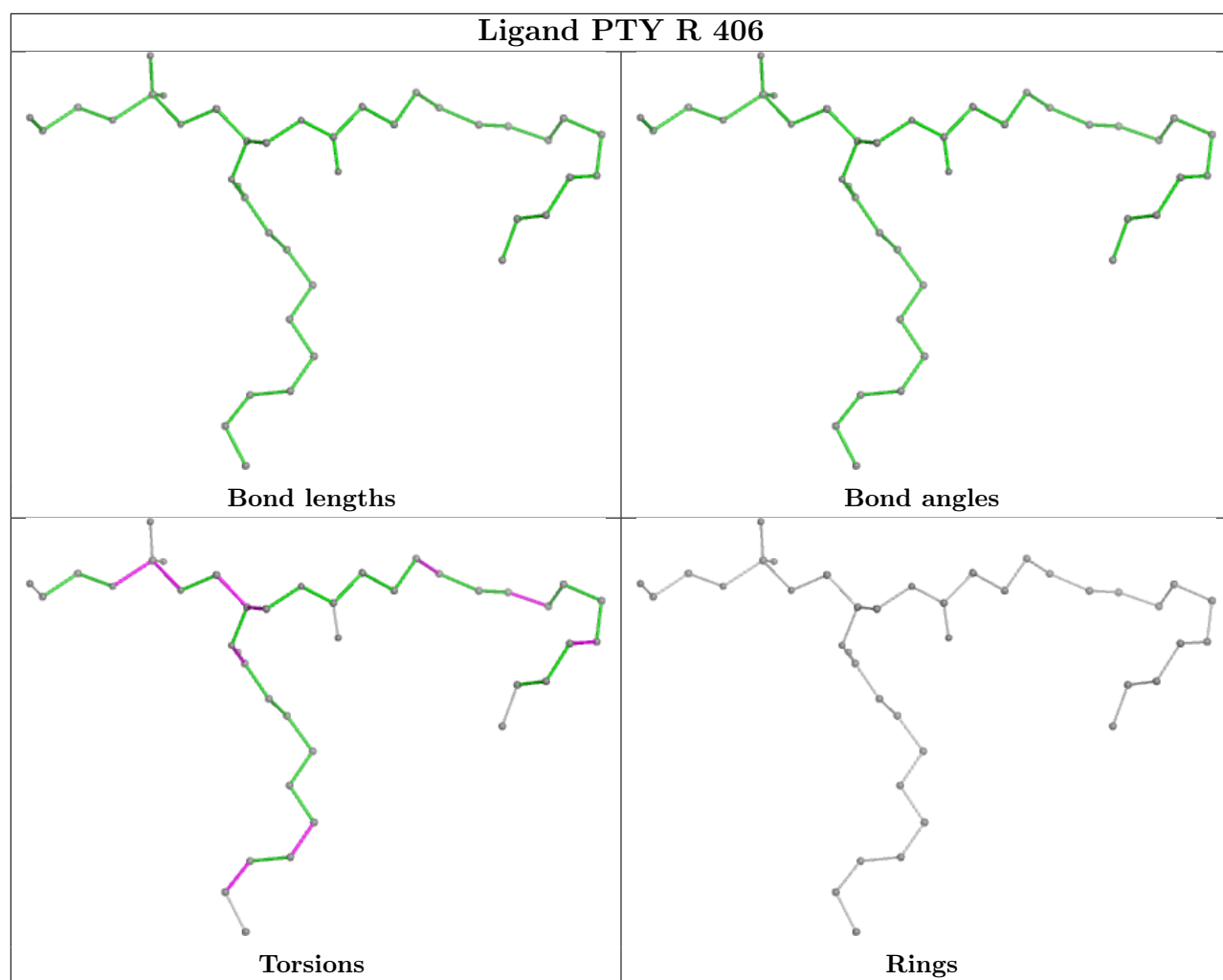


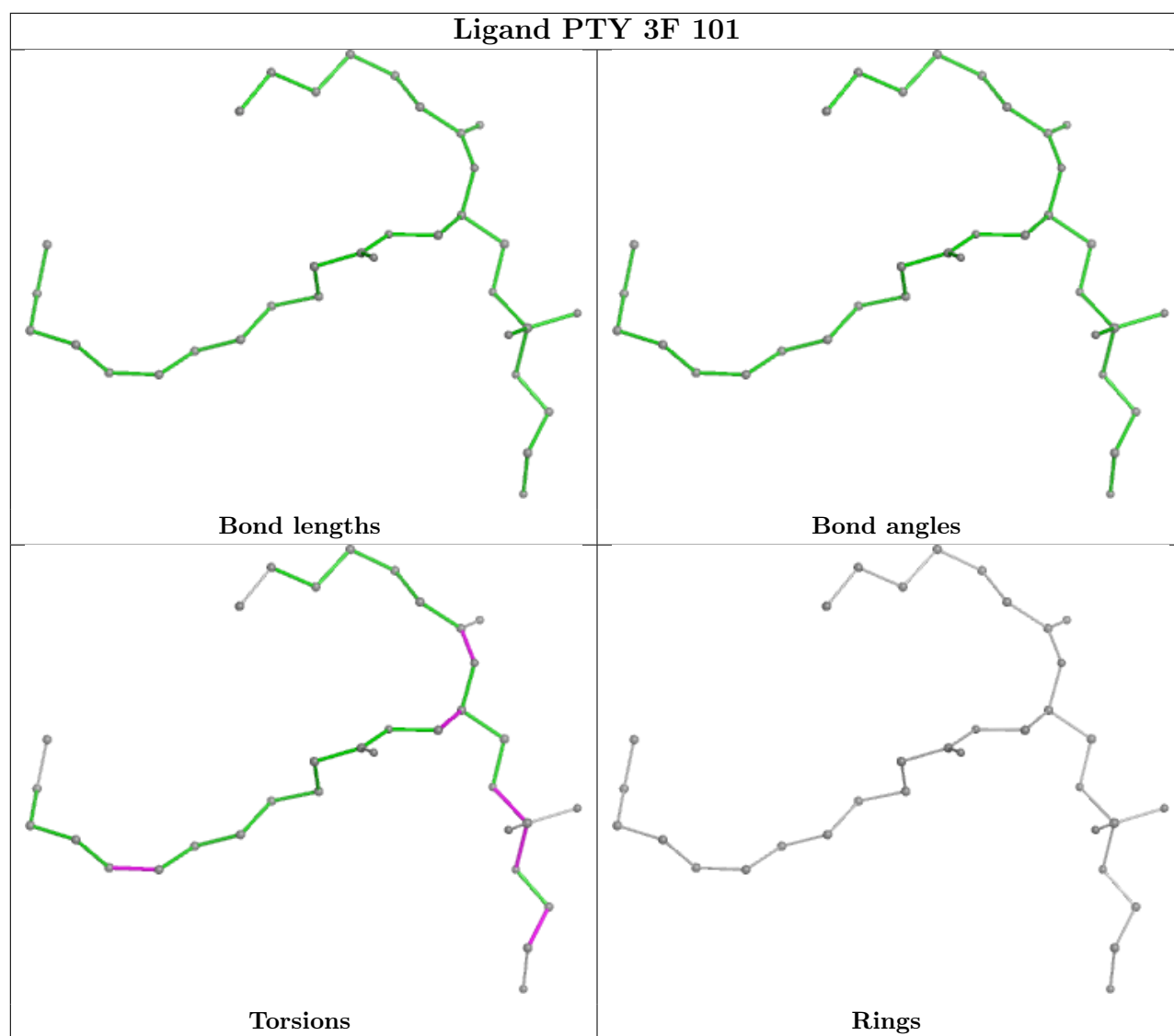


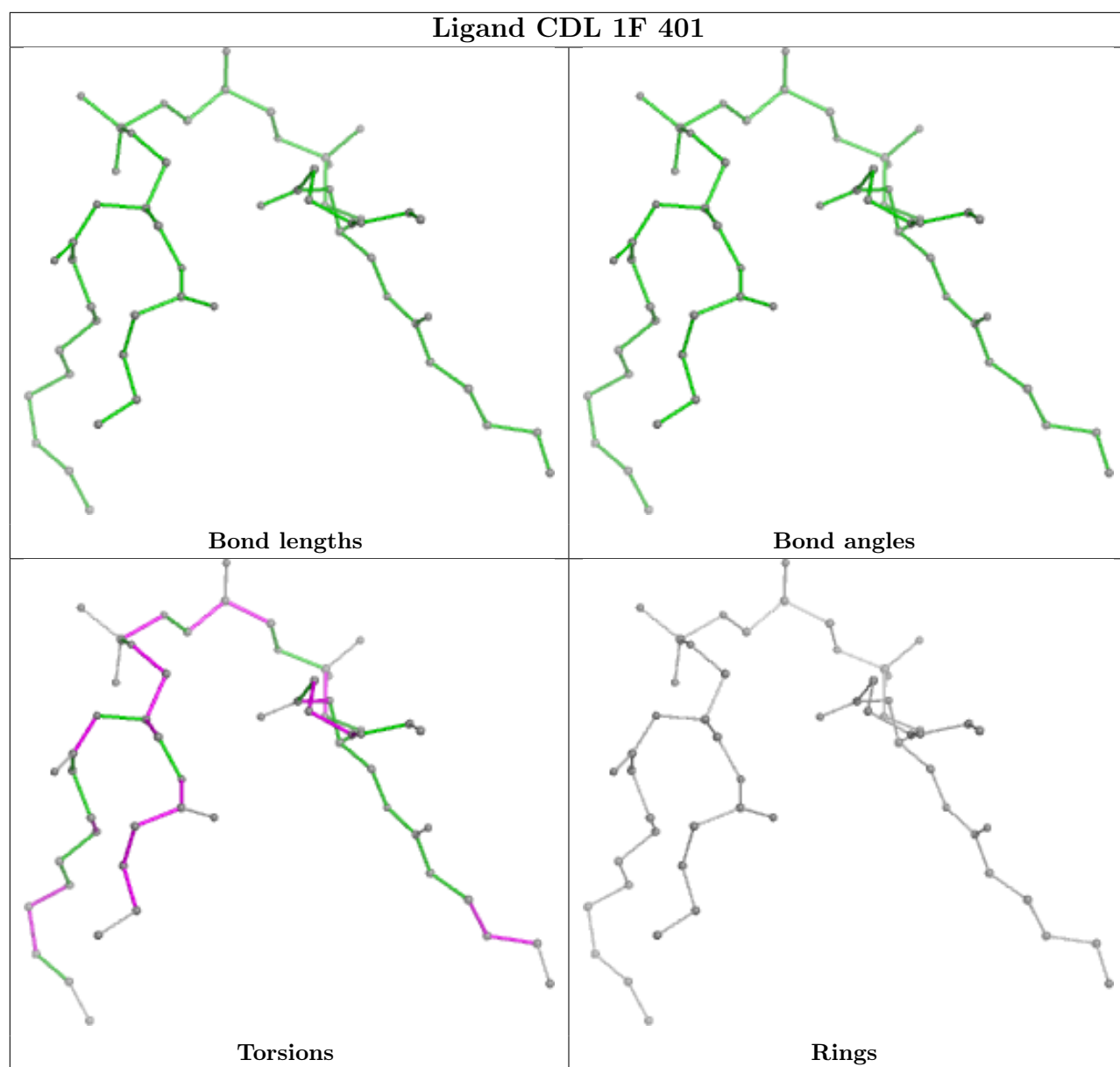


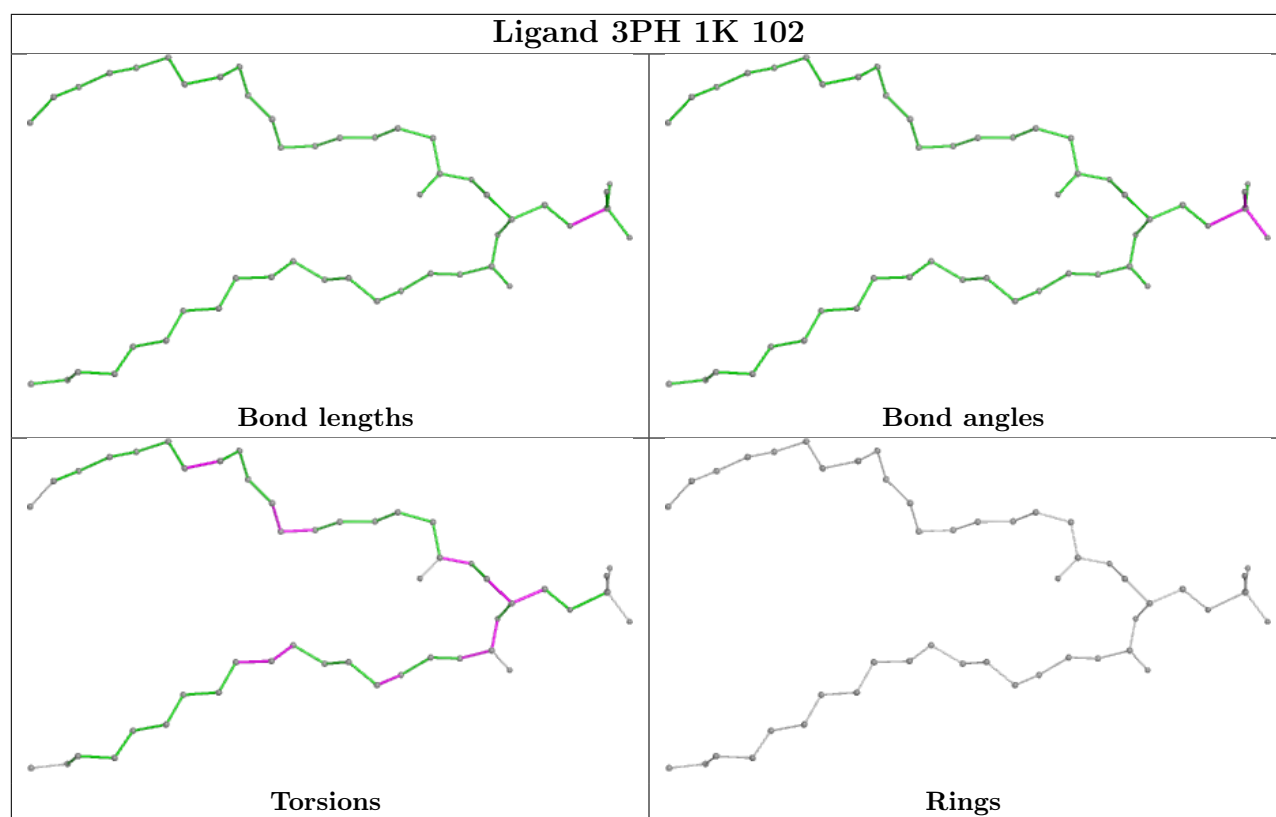












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50202. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

This section was not generated.

6.2 Central slices [i](#)

This section was not generated.

6.3 Largest variance slices [i](#)

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

This section was not generated.

6.5 Orthogonal surface views [i](#)

This section was not generated.

6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.